us-09-899-718a-1.oli.rge

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PAT 06-FEB-2002
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AX32580 Sequence
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AX32582 Sequence
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AX32584 Sequence
AX3264 Sequence
                                                                                                        AB019623 Triticum
AF2110373 Triticum
AF286320 Triticum
AF110375 Aegilops
AX349066 Sequence
AF250137 Triticum
AX32803 Sequence
AX325804 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
                                                     AF113843 Triticum
AB029064 Triticum
AF113844 Triticum
AF163319 Triticum
                    AB029061 Triticum
AB029063 Triticum
X57233 Wheat waxy
                                                                                                  AB029062 Triticum
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Sprunck, S., Kluth, A., Becker, D., Luetticke, S. and Loerz, H.
Sprunck, S., Kluth, A., Becker, D., Luetticke, S. and Loerz, H.
Promoters of gene expression in plant caryopses
Patent: WO 0202785-A 1 10-JAN-2002;
Aventis CropScience GmbH (DE)
Location/Qualifiers
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/organism="Triticum aestivum"
/db_xref="taxon:4565"
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Sequence 1 from Patent W00202785.
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AF250137
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AB073159
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                   bread wheat.
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JOURNAL
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AX349063
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                                                                          July 31, 2002, 12:12:23 ; Search time 4552.47 Seconds (without alignments) 17398.674 Million cell updates/sec
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Gapop 60.0, Gapext 60.0
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3785
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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ry Match t. 100.08; Score 3785; DB 6; Length t. Local Similarity 100.08; Pascar No.0; Indels 1 gritiggitticgetytttcattcettcttcttaagggtaataccat. 1 gritiggitticgetytttcattcettcttcttaagggtaataccat. 1 gritiggitticgetytttcattcettcttcttaagggtaataccat. 1 gritiggittil
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Qy Db	1081	ggactggctagctatactaccgtgtaacactagtacgttggtgt
Qy	1141	aggtgccacagactagtattt
QY	1201	togtaggacgaaaaoggtcatatatgtggcactggccttctagagactctccaagaggct 1260
Qy	1261	caccacttcaccftgagtgacagccaccgtcgcgtaaaccacgcatttacgtttcccc 1320
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QY	1381	acgcgccggtttggcagcacgtacgtgctagctgttcat
QY	1441	agcaaaagaga
QY Db	1501	aggaagcaatcccgggccatgcagcgccattgccacgccccagcgaaaagcgaaggcgag 1560
Qy Db	1561 1561	agcgagagcaca
QY	1621 1621	agcaggaacaccaccggcagccc
QY Db	1681 1681	agaagatgegtgcacggccggccggcaggaagggggcgcgccggccggc
QY	1741	aaagggggttggccagccacgacgccgtggaaagg
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QY	1861 1861	cgctcggcacgcacgcaggcaggcagaacaaacaaacaaa
QY Db	1921 1921	ctccactcaacgtcgcctttcaggacgatgcttcggtg
Oy Db	1981	tctatgacatgtgagcccaacagatggctggcccacatgt
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tgccgtcccgtctaggcgttcggtgccgcgtgcatgcatg	CCCACACACTACAACCAGGAGCCTCGATCTGCCAGTGAAGAAGAAGAAGAAGAACTCAC atgcccggccggcgactgtgagtacgctcccgtccaggaagaagaagaagaagaa	aggtcggttggtctagtagtagatagatccaaccaaatgccgccatgttgttagatccag	tagatttaaaatcatgtaaaaattaaaaaaaagatttaaaatcatgtactgctagcta	gcctaggttaattacgactagacagagcataatgcgcataaacatttctgttt 	tttggcgtgggcgttccactgcacctacagaacaaattccatttctcagccagttccacllllllllll	actctggtcatgttaatttggatttcaaattcaaatgtaaaatccagaaaacttgactgc 	gccacacctgcgcgcatggcggtctggtcacgtccagctcgccacctccggcac
10 10 16 22 28 28	2281 2341 2341 2401 2401 2461	2521 2521 2581 2581	2641 2641 2701 2701	2761 2761 2821 2821	2881 2881 2941 2941	3001 3001 3061 3061	3121 3121 3181
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1 (sites)
Murai,J., Taira,T. and Ohta,D.
Isolation and characterization of the three Waxy genes encoding the granule-bound starch synthase in hexaploid wheat Gene 234 (1), 71-79 (1999)
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AB019622 2805 bp DNA linear PLN 05-AUG-199
Triticum aestivum gene for starch synthase (GBSSI), complete cds.
AB019622
                                                                                                                                                                                                                                                                                                                                                                                                Murai, J. Taira, T. and Ohta, D.

Murai, J., Taira, T. and Ohta, D.

Direct Submission

Submitted (10-NoV-1998) Jun Murai, Osaka Prefecture University,

College of Agriculture; 1-1 Gakuen-cho, Sakai, Osaka 599-8531,

Japan (E-mail: Junki@demeter.plant.osakafu-u.ac.jp,

Tel:81-722-54-9409, Fax:81-722-54-9409)

Location/Qualifiers

1. 2805
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/db_xref="taxon:4565"
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starch synthase (GBSSI)
Triticum aestivum DNA.
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/sub_species="dicoccoidés"
| db_xref="taxon:8559"
| join(1. .321,404 . 484,569 . 667,777 . .930,1056 . .1156,
| 1256 . .1609,1701 . .1880,1976 . .2167,2258 . .2344,2443 . .2571,
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256. .1609,1701. .1880,1976. .2167,2258. .2344,2443. .2571,
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Vgasaapkosrkpherdreclsmvyratgsggmilyevgabaapwsktgelcdbylggl
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HPCFLEKVRGKYTKET IGPDAGTDYEDNQORFSLLCQAALEVPRILDLNNNPHFSGPY
GEDVVFVCNDWHTGLLACYLKSNYQSNGIIRTRAKVAFCIHNISYQGRESFDDFAQLNL
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NIMMLTGITGIYUGMDYSEMDPIKDRELTVWYDVTPALEGRALUAEGGEALGCGELPVDR
KVPLVAFIGHLEEQGREDVMTAAIPELYEEDGYULLGGFKKFRERLLKSVEERFPT
KVRAVVRFNAFLAELAGAMAGADPLATTSRFEFCGLIOLQGMRYGTPCACASTGGLYDTI
VEGKTGFHMGRLSVDCNVVEPADVKKVVTTLKRAVKVVGTPAYHEMVKNCMIQDLSWT
                                                                                                             PLN 27-JAN-2001
                                                                                                                             Triticum turgidum subsp. dicoccoldes waxy gene for starch synthase (GBSSI), complete cds.
AB029061
                                                                                                                                                                                                              starch synthase (GBSSI).
Triticum turgidum subsp. dicoccoides (sub_species:dicoccoides) DNA.
Triticum turgidum subsp. dicoccoides
                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                  Murai,J., Taira,T. and Ohta,D.

Splation and characterization of the four Waxy genes encoding the splation and characterization of the four waxy genes encoding the splanule-bound starch synthase in tetraploid wheats ppl. Biol. Sci. (1999) In press

C (bases I to 2781)

Murai,J., Taira, 2781)

Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-JUN-1999) Jun Murai, Osaka Prefecture University, College of Agriculture; 1-1 Gakuen-cho, Sakai, Osaka 599-8531, Japan (E-mail:junki@demeter.plant.osakafu-u.ac.jp, Tel:81-722-54-9409, Fax:81-722-54-9409)

Location/Qualifiers
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    601 CGAGAGGGTGAGGTACTTCCACTGCTACAAGCGCGGGGGTGGACCGCGTGTTCGTCGAC 658
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                                                                                                             2781 bp
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                                                                                  join(13. .333,416. .496,581. .679,789. .942,1068. .1168,
.268. .1621,1713. .1892,1988. .2179,2270. .2356,2455. .2583,
                                                                                                                                                                                                                                                      /translation="maalvysqlatsgtvlsvydrfrrpgegglrprnpadaalgmry
VGASAAPKQSRKPHREDRRCLSMVVRATGSGGMNLVFVGAEMAPWSKTGGLGDVLGGL
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HPCFLEKVRGRTWETTYGPDAGTVSPDNQDFSLLCQAALEVPRILDLNNNPHFSGFV
GEDVVFVCNDWHTGLLACYLKONYQSNGIYRTAKVAFCIHNISYQGRFSFDDFAQLNL
PDRFKSSFDFIDGYDKPVEGRKINMMRAGILQADKVLTVSFYYAEELISGEARGCELD
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KVPLVAFIGRLEEGKGPDVMIAAIPEIVKEEDVQIVLLGTGKKKFERLLKSVEEKFPT
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/protein_id="BAA77350.1"
/db_xref="GI:4760580"
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+ive 0; Mismatches
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/organism="Triticum turgidum subsp. durum"
/db xref="taxon:4567"
join[1. 321,404. 484,569. .667,777. .930,1056. .1156,
1256. .1609,1701. .1880,1976. .2167,2258. .2344,2443. .2571,
2665. .2781)
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join(1. 321,404. 484,569. 667,777. 930,1056. 1156,
1256. 1609,1701. 1880,1976. 2167,2258. 2344,2443. 2571,
2665. 2781)
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Triticum durum waxy gene for starch synthase (GBSSI), complete cds.
AB029063
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Triticum durum DNA.
Triticum turgidum subsp. durum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
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                                                                                                                      ttcgtcggcgccgagatggcgccctggagcaagactggcggcgtcctcggcgacgtcctcggg 3439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-JUN-1999) Jun Murai, Osaka Prefecture University, College of Agriculture; 1-1 Gakuen-cho, Sakai, Osaka 599-8531, Japan (E-mail:junkiedemeter.plant.osakafu-u.ac.jp, Tel:81-722-54-9409; Fax:81-722-54-9409)
TGCAGCCATGCCTGCCGTTACAACGGGTGCCGTGTCCGTGCAGGCCAACGGTCACCGGGT 420
                                                                                                                                      gaccggcggtgcctctccatggtggtgcgcgccacggggcagcggcgtgaacctcgtg
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Isolation and characterization of th
gradule-bound starch synthase in tet.
Appl. Biol. Sci. (1999) In press
2 (bases it to 2781)
Murai, J., Taira, T. and Ohta, D.
Direct Submission
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BAMAANGHTWAVI SPRYDOYKDAWDTSVISEIKVVDRYERVYRYFHCYKRGVDRVFVD
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KVPLVAFIGITGTVNGNDSSEMPPINDRFLTVWEEDVQIVLLGGTGKKKFFRLLKSVEEKFPT
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VEGKTGFHMGRLSVDCNVVEPADVKKVVTTLKRAVKVVGTPAYHEMVKNCMIQDLSWR
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Submitted (04-DEC-1990) J.R. Clark, WYE COLLEGE, UNIVERSITY OF
LONDON, DEPT OF BIOCHEMISTRY & BIOLOGICAL SC., NR. ASHFORD KENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3441 goctcoccgocgcgatggcogtaagcttgcgccactgccttcttataaatgtttcttcct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3681 actttactgactggctggatctcgcagatcaaggtcgttgacaggtacgagagggtgagg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.3%; Score 465; DB 8; Le
100.0%; Pred. No. 1.1e-245;
ive 0; Mismatches 0;
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                              /protein_id="BAA88511.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              фq
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TITLE
JOURNAL
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TN25 5AH, UK

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PHPCFLEKVRGKTKEKIYGPDAGTDXEDNQQRFSLLCQAALEVPRILDLNNNPHFSGFY
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ISGEARGCELDNIMRLIGITGIVNGMDYSEWDPINBRELTVNYDVTAALEGRALNKEA
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CASTGGLYDTIVGEKTGFHMGRLSVDCNNVVEADVKKVVTILKRAVKVVGTPAYHEMV
KNCMIQDLSWKGPAKNWEDVLLELGYGESEPGIVGEEIAPLALENVAAP"
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2 (bases 1 to 2186)
Clark,J.R., Robertson,M. and Ainsworth,C.C.
Nucleotide sequence of a wheat (Triticum aestivum L.) cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             egecetiggageaagactggeggeeteggegaegteeteggggggeeteeeegeegeeatgg 3458
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                                                                                           Erratum:[[published erratum appears in Plant Mol Biol 1991
Oct;17(4):957]]
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                                                        encoding the waxy protein
Plant Mol. Biol. 16 (6), 1099-1101 (1991)
91322506
                                                                                                                                                                                                   'organism="Triticum aestivum"
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                                                                                                                                                                                                                                                                             /cell_line="Chinese spring"
/tissue_type="endosperm"
/clone_lib="lambda gt10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                      /chromosome="7A, 7B, 4B"
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                                                                                                                                                                                                                                                                                                                                                                               /evidence=experimental
1. .2186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="waxy"
/EC_number="2.4.1.11"
                                                                                                                                                                                                                   /db_xref="taxon:4565"
                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                              /gene="waxy"
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ERVRYFHCYKRGVDRVFVDHPCFLEKVRGKTKEKIYGPDAGTDYEDNQQRFSLLCQAA
LEPPRILDINNNPHFSGPYGEDVYFVONDWHFGLLACYLKSNYGSNGIYRTAKVAFCT
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GRAKREPELLLEKSVEEKFPTYKVRAVYRFRAPLAHGMAGADVLATYSTERECLIOLOG
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TPAYHEMYKNCMIQDLSWKGPAKNWEDVLLELGVEGSEPGIVGEEIAPLALENVAAP"
                                                                                                                                        PLN 20-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (dases 1 to 1801)
Vrinten, P.L. and Nakamura, T.
Urinter, E. and Nakamura, T.
Direct Submission
Submitted (14-DEC-1998) Crop Breeding, Tohoku National Agricultural
Experiment Station, Shimo-Kuriyagawa, Morioka, Iwate 020-01, Japan
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MAALVTSQLATSGTVLSVTDRFRRPGFGGLRPRNPADAALGIRT
VGASAAPKQSRKPHRGNRRCLSMVANGHRVMVISPRYDQYKDAMDTSVISEIKVVDRY
                                                                                                                                                                                                                                                                                        Triticum aestivum
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
                                                                                                                                        AF113843 1801 bp mRNA linear PLN 20-APR-19:
Triticum aestivum granule-bound starch synthase precursor (Wx-Al)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Non-functional Wx-Alb allele of waxy wheat; sportaneously mutated Wx-Al gene" 32. 1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="granule-bound starch synthase precursor"
/protein_id="AAD26155.1"
/db_xref="GI:4588607"
                                                                                                                                                                                                                                                                                                                                                                                                    Aclecular characterization of waxy mutations in wheat Mol. Gen. Genet. 261 (3), 463-471 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 156; DB 8; Length 1801;
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Vinten, P., Nakamura, T. and Yamamori, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Triticum aestivum"
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ive 0; Mismatches
                                                                                                                                                                                    mRNA, Wx-Alb allele, complete cds AF113843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cultivar="Waxy"
/db_xref="taxon:4565"
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/note="Waxy protein"
/codon_start=1
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bread wheat.
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                                       383 CCG 385
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JOURNAL
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MALVYSQLATSGTVLGITDRFRRAGFOGVRPRNPADAALVMRT
| CAAAAANCGRKAHGGSRCLSMVVRATGSGGMLVFVGAEMAPWSKTGGLGDVLGGL
| PAAAAANGHRVWVISPRYDQYKDAMDTSVVSBIKVADAERRRYFHCYKRGVDDRFVDD
| PPOLETEKVRGKTKEKINGSPROINDSTRONGLRFSLLCQAALEAFRILDLNNNPPFSGFV
| GEDVVFVCNDWHTGLLACYLKSNOSMGITWTAKVAFCIHNISYQGRFSFDDFAQLNL
| PDRFKSSFDPIDGYDKPVEGRKINWMKAGILQADKVLTVSPYYAFEBLISGERANKEELD
| NIMRLIGITGIVNGMVYSGRDPTKDFFLAVWTDYTTALEGRALNKEALQASVGLPVDR
| KVPLVAFIGRLEGGKGPDVMIAATEBILKEEDQIYLLGTGKKKFFERLLKSVEEKFPN
| KVRAVYFRARLAHOMAGADVLAYTSRFEFCGLIQLQGMRYGTPATGGKGLVDTI
| VEGKTGFHMGRLSVDCNVFCAPATTSRFEFCGLIQLQGMRYGTPATGGLUDTI
| VEGKTGFHMGRLSVDCNVFCAPATTSRFEFCGLIQLQGMRYGTPATGGLUDTI
| VEGKTGFHMGRLSVDCNVFCAPATTSRFEFCGLIQLQGMRYGTPATGMVKNCMIQDLSWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Triticum turgidum subsp. durum"
/db_xref="taxon:4567"

join(1. .321.418. .498,590. .688,799. .952,1093. .1193,

1253. .1666,1731. .1910,1993. .2184,2265. .2351,2439. .2567,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(1. .3<u>2</u>1,418. .498,590. .688,799. .952,1093. .1193,
1293. .1646,1731. .1910,1993. .2184,2265. .2351,2439. .2567,
2688. .2804)
                                                                                                                       Triticum durum waxy gene for starch synthase (GBSSI), complete cds. AB029064
                                                                                                                                                                                                                                                                                                                                1 (sites)
Murai,J., Taira,T. and Ohta,D.
Musal,J., Taira,T. and Ohta,D.
Scolation and characterization of the four Waxy genes encoding the granule-bound scharch synthase in tetraploid wheats
Appl. Biol. Sci. (1999) In press
2 (bases 1 to 2804)
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                                                                                                                                                                                                                                          Triticum turgidum subsp. durum
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mural, J., Taira, T. and Ohta, D.
Direct Submission
Submitted (16-JUN-1999) Jun Murai, Osaka Prefecture University,
College of Agriculture; 1-1 Gakuen-cho, Sakai, Osaka 599-8531,
Japan (E-mail:junki@demeter.plant.osakafu-u.ac.jp,
Tel:81-722-54-9409, Fax:81-722-54-9409)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.5%; Score 93; DB 8; L
100.0%; Pred. No. 2.7e-39;
tive 0; Mismatches 0;
                                                                                                                     DNA
121 GAGGCCCCGGAACCCGGCGGATGCGGCGCTCGGCAT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 580 t
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/db_xref="G1:6624287"
                                                                                                                2804 bp
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VERSION
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                                                                RESULT
AB029064
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AF113844

RESULT

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PLN 20-APR-1999
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VGASAAPTOSRKAHRGTRRCLSMVVRATGSGGMNLVFVGAEMAPWSKYGGLGDVLGGL
PPAMAANGHRVMVISPRYDQYKDAWDTSVVSEIKVVDKYERVRYFHCYKRGVDRVFVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HCFLEKYRGKIKEKITGPDAGTDYEDNQORFSLLCQAALEYPRILANDANBYFSGFY
GEDVYFYCNDWHTGLLACYLKSNYQSNGIYRAAKVAFCIHNISYQGRESFDDFAQLND
BDFKSSEPFIOGYDKPYSGRKINWMKAGILQADKVLTVSPYYAEELISGEARGCELD
NIMRLIGITGIVNGMDYSEMDFYNDRYFALNYNDITTALEGKANKREALQAEUJEVDR
KYPLYAFIGKLEEDQAGFPYMIAAIPEILKEEDYQIVLLGTGKKRFERLLKSIEEKFPS
KVRAVVRFNAPLAHQMMAGADVLAVTSRFEPCGLIQLGGMRYGTPACAASTGGIYUTI
VEGKTGFHMGRLSYDCNYVEPADVKKVYTLKRAVKVVGTPAYTEMWKNCMIQDLSWK
                                                                                                                                                                                                      Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Dooideae; Triticae; Triticae. Triticae. Triticae. Vornten, P., Nakamura, T. and Yamamori, M. Wolcular characterization of waxy mutations in wheat Mol. Gen. Genet. 261 (3), 463-471 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                     2.24.00.7
2. (bases 1 to 2028)
Vrinten,P.L. and Nakamura,T.
Direct Submission
Submitted (14-DEC-1998) Crop Breeding, Tohoku National Experiment
Station, Shimo-Kuriyagawa, Morioka, Iwate 020-01, Japan
  AF113844 2028 bp mRNA linear PLN 20-APR-19
Triticum aestivum granule-bound starch synthase precursor (Wx-Dl)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="Wx-Dl"
/note="Wx-Dlb null allele of Waxy wheat; spontaneously
mutated Wx-Dl gene"
/allele="Wx-Dlb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3111 getgcaggtagccacaccctgcgcgcgccatggcggctctggtcacgtcccagctcgcca 3170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="granule-bound starch synthase precursor"
/protein_id="AAD26156.1"
/db_xref="GI:4588609"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Waxy protein; non functional"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Triticum aestivum"
                                                     mRNA, Wx-D1b allele, complete cds. AF113844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cultivar="Waxy
                                                                                                           AF113844.1 GI:4588608
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Best Local Similarity 100.c
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                                                                                                                                                   bread wheat.
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AF113844
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join(1. 324,424. .504,593. .691,805. .958,1092. .1192,
1262. .1615,1708. .1887,1974. .2165,2249. .2335,2433. .2561,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(1. .324,424. .504,593. .691,805. .958,1092. .1192,
[262. .1615,1708. .1887,1974. .2165,2249. .2335,2433. .2561,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DHPCFLEKVRGKTKEKIYGPDAGTDYBDNQLRFSLLCQAALEAPRILDLNNNPYFSGP
YGEDVYFVCNDRHTGLLACYLKSNYQSSGIYRTAKVAFCIHNISYQGRFSFDDFAQLN
LPDRFKSSFDFIDGYDKPVEGRKINWMKAGILQADKVLTVSPYYAEELLSGEARGCEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNIMRLTGITGIYNGMDVSEMDPAKDKFLAANYDVITALEGKALNKEALQAEVGLPVD
RKVPLVARFGRLEEQKGPDVMIAAIPEILKEEDVQIVLLGIGKKKFERLLKSVEEKFP
SKVRAVVRFNAPLAHQMMAGADVLAVISRFEPCGLIQLQGMRYGIPCACASTGGLVDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="maalvtsolatsgtvlgitdrprragpggvrprspadplgmrt
tgasaapkqqsrkahrgtrrclsmvvratgsagmnlvfvgaemapwsk7gglgdvlgg
lppamaanghrymvlspryddykDamdtsvvselkvadeyervrfhcykrgvdrvfy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IVEGKTGFHMGRLSVDCNVVEPADVKKVVTTLKRAVKVVGTPAYHEMVKNCMIQDLSW
KGPAKNWEDVLLELGVEGSEPGVIGEEIAPLAMENVAAP"
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                            Murai,J., Taira,T. and Ohta,D.
Isolation and characterization of the four Waxy genes encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABO19623 2818 bp DNA linear PLN 05-AUG-19
Triticum aestivum gene for starch synthase (GBSSI), complete cds.
AB019623
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                                                                                                                                                                                                                                                                  Submitted (16-JUN-1999) Jun Murai, Osaka Prefecture University, College of Agriculture: 1-1 Gakuen-cho, Sakai, Osaka 599-8531, Japan (E-mail:junki@demeter.plant.osakafu-u.ac.jp, Tel:81-722-54-9409) Eax:81-722-54-9409) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              /organism="mriticum turgidum subsp. dicoccoides"
/sub_species="dicoccoides"
/db_xref="taxon:85692"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.0%; Score 77; DB 8; Length 2793; 100.0%; Pred. No. 2.1e-30; ative 0; Mismatches 0; Indels
                                                                                                                                              granule-bound starch synthase in tetraploid wheats Appl. Biol. Sci. (1999) In press 2 (bases 1 to 2793)
Murai,J., Taira,T. and Ohta,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="starch synthase (GBSSI)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="BAA88510.1"
/db_xref="G1:6624283"
                                                       Pooideae; Triticeae; Triticum.
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Triticum aestivum DNA.
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Matches 77; Conserva
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                                                                                                                                    TITLE
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Triticum turgidum subsp. dicoccoides (sub_species:dicoccoides) DNA.
Triticum turgidum subsp. dicoccoides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEDVYFVCNDWHTGLLACYLKSNYOSNGIYRAAKVAFCIHNISYOGRFSFDDFAQLNL
PDRRKSSFDFIDGYDKPVEGRKINWMKAGILQADKVLTVSPYYAEELISGEARGCELD
NIMRLTGITGIVNGMDVSEWDPTKDKFLAVNYDITTALEGKALNKEALQAEVGLPVDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="maalvtsQlatsgrvlgitdrfrragfoggvrprspadalgmrt
vgasaptgsrkahrgtrrclsmvvratgsggmnlvfvgaemapwsktgglcbvlggl
ppamaanghrvmvisprydgykdamdfsvvseikvvdkyervrfhcyrkgvdrrfyv
hpcflekvrgktrekiygpdagtdyednogrsllcqaaleyriinldnnpyfsgpy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVRAVVRENAPLAHQMMAGADVLAVTSREEPCGLIQLQGMRYGTPCACASTGGLVDTI
VEGKTGFHMGRLSVDCNVVEPADVKKVVTTLKRAVKVVGTPAYHEMVKNCMIQDLSWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KVPLVAFIGRLEEQKGPDVMIAAIPEILKEEDVQIVLLGTGKKKFERLLKSIEEKFPS
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Submitted (28-JUN-1999) Crop Breeding, Tohoku National Agricultural
Experiment Station, Akihira 4, Morioka, Iwate 020-0198, Japan
                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
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                                                                                                                                                         1 (bases 1 to 2127)
Vrinten, P.L. and Nakamura, T.
Wheat granule-bound starch synthase I and II are encoded by
separate genes that are expressed in different tissues
plant physiol. 122 (1), 255-264 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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617 c 687 q 371 t
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100.0%; Pred. No. 2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Triticum aestivum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cultivar="Chinese Spring"
/db_xref="taxon:4565"
/chromosome="7D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="immature seed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAF34135.1"
/db_xref="G1:6969978"
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                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 2127)
Vrinten, P.L. and Nakamura, T.
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Matches 77; Conservative
                                                                             Triticum aestivum
                                                    bread wheat.
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1274. .1627,1720. .1899,1986. .2177,2262. .2348,2446. .2574,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Join(13. .336,436. .516,605. .703,817. .970,1104. .1204,
[274. .1627,1720. .1899,1986. .2177,2262. .2348,2446. .2574,
Mrai,J., Taira,T. and Ohta,D.
Solation and characterization of the three Waxy genes encoding the
Tranule-bound starch synthase in hexaploid wheat
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TGASAAPKQQSRKAHRGTRRCLSMVVRATGSAGMNLVFVGAEMAPWSKTGGLGDVLGG
LPPAMANAIGRRVMVISPRYDOXKDAWDTSVVSBIKVANDEYBERVRYFRCYKRGVDRVFV
DHPCFLEKVRRGKTREKIYGPDAGTDYEDNQLFFSLLCQAALEAPRILDLNNNPYFSGP
VGEDVVFVCNDWHTGLLACYLKSNYQSSGIYRTAKVAFCIHNISYGGRESFDDFAQLB
LPDRFKSSFDPIDGYDKPVEGRKINWMKAGILQADKVLTVSPYYAEELISGEARGCEL
DNIMRLIGITGIVNGMDYSEMDPARDKETAANTOYTTALEGRALNKERLQAEVGLPVD
RKVPLVAFIGILEGRGEDVMIAAIPBILKSVEEKFP
SKVRAVVRFNAPLAHQMMAGADVLAVTSRFEDCGLIQLGGGKKKFFERLLKSVEEKFP
LMEGKTGGHMGRLSVDCNWYBEADKKVVTTLKRAVKVVGTPAYHEWVRNCHIQDLSW
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
1 (bases 1 to 2834)
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                                                                                                                                                                                           Submitted (10-NOV-1998) Jun Murai, Osaka Prefecture University, College of Agriculture: 1-1 Gakuen-cho, Sakai, Osaka 599-8531, Japan (E-mail:junki@demeter.plant.osakafu-u.ac.jp, Tel:81-722-54-9409, Fax:81-722-54-9409)
Location/Qualifiers
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846 c 828 q 565 t
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/product=starch synthase (GBSSI)"
/protein_id="BAAA73551.1"
/db_xref="GI:4760582"
                                                                                                                                                                                                                                                                                                                                            /organism="Triticum aestivum"
/db_xref="taxon:4565"
                                                                                                                                                 Murai, J., Taira, T. and Ohta, D. Direct Submission
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                                                                             Gene 234 (1), 71-79 (1999)
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Matches 77; Conservative
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/organism="Triticum monococcum"
/cultivar="A0S 22986"
/db_xref="traxon:4568"
join(<32. .355,444 .524,613. .711,830. .983,1127. .1227,
1309. .1662,1752. .1931,2013. .2204,2288. .2374,2474. .2602,
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1309. .1662,1752. .1931,2013. .2204,2288. .2374,2474. .2602,
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DINBLIGTGIVOMMYSENDPTKDRFLTVANYTALEGRYUNKRALQABVGLPVD

RKVPLVAFIGTEGROKGPDVALAAIPEIVENEDVOIVLGTGKKKFFRLLIKSVEBFP

SKVRAVVRFNAPLAHOMMAGADVLAVTSRFEDCGLIQLOGGMYGTPCACASTGGLVD

IVEGKTGFHMGRLSVDCNVVBPADVKKVVTTLKRAVKVVGTPAYHEMVKNCMIQDLSW

1956KTGFHMGRLSVDCNVVBEPADVKKVVTTLKRAVKVVGTPAYHEMVKNCMIQDLSW

834 C 831 9 591
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VGASAAPKQQSRKAHRGTRRCLSVVVRATGSGGMNLVFVGAEMAPWSKTGGLGDVLGG
LPPAWAANGHRVMVISPRYDQYKDAMDTSVVSEIKVADEYERVRYFHCFKRGVDRVFV
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Genome (1999) In press 2 (bases 1 to 2834)
2 (bases 1 to 2834)
Part. L. Bhave, M., Fairclough, R., Konic, C., Rahman, S. and Appels, R. Direct Submission
Submisted (02-DEC-1998) School of Life Sciences and Technology, Victoria University of Technology, Werribee Campus, PO Box 14428
MCMC, Melbourne, Victoria 8001, Australia
Location/Qualifiers
1 1. 2834
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Pred. No. 2.1e-30;
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/db_xref="G1:6318538"
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/gene="wx-TmA"
<32. .>>
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1.8%; Score 69; DB 8;
100.0%; Pred. No. 5.7e-2
tive 0; Mismatches
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/note="Oligonucleotide"
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/note="GBSSI"
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                                                                                     FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae; Triticeae; Aegilops.

( pases 1 to 2893)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 2893)
Yan,L., Bhave,M., Fairclough,R., Konic,C., Rahman,S. and Appels,R.
                                                                                                          Submitted (11-JUL-2000) United States Department of Agriculture, Agricultural Research Service, 800 Buchanan Street, Albany, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3543 gccaacggtcaccgggtcatggtcatctccccgcgctacgaccagtacaaggacgcctgg 3602
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Expression, and Homolog Assignment by Diffferential PCR
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204. .2021
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                                                                                                                                                                        Location/Qualifiers
1. .2289
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                         Unpublished
2 (bases 1 to 2289)
McCue, K.F. and Anderson, O.D.
                                                                                                                                                                                                                                                                                                                              /gene="GbssI"
204. .2021
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                                                                                                                                                                                                                                                                                                                                                                               /gene="GbssI"
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Aegilops tauschii
                                                                                          Direct Submission
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AUTHORS
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                                                                         AUTHORS
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join(32. 352,443. 523,620. 718,823. 976,1128. 1228,
1370. 1723,1809. 1988,2071. 2262,2347. 2433,2532. 2660,
2777. 2893)
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Submitted (02-DEC-1998) School of Life Sciences and Technology, Victoria University of Technology, Werribee Campus, PO Box 14428 MCMC, Melbourne, Victoria 8001, Australia Location/Qualifiers
                                                                                                                                                                                                                                                                                                   /product="granule-bound starch synthase WX-TtD protein"
/protein_id="AAF06938.1"
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Sprunck, S., Kluth, A., Becker, D., Luetticke, S. and Loerz, H. Promoters of gene expression in plant caryopses
Patent: WO 0202785-A 4 10-7AN-2002;
Aventis CropScience GmbH (DE)
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20 c 15 a BASE COUNT ORIGIN

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0; Gaps Query Match 1.8%; Score 68; DB 6; Length 72; Best Local Similarity 100.0%; Pred. No. 1.6e-25; Matches 68; Conservative 0; Mismatches 0; Indels

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QY 1996 cccaacag 2003 ||||||||| Db 61 CCCAACAG 68

Search completed: July 31, 2002, 16:11:39 Job time: 14356 sec

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Run on:

Sequence 10, Appl Patent No. 5457089 Sequence 16, Appl Sequence 17, Appl

Sequence Sequence Sequence Sequence Sequence 1, Appli 1, Appli 1, Appli 2, Appli 81, Appli 4, Appli

Sequence 2 Sequence

Appli

Sequence Sequence Sequence Sequence Sequence Sequence

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"WELLO, Particia Ann Owens
"WELLO, Lining
APPLICANT: Guo, Lining
APPLICANT: Skokut, Thomas A.
APPLICANT: Folkerts, Otto
APPLICANT: Folkerts, Otto
APPLICANT: Folkerts, Otto
TITLE OF INVENTION: COMPOSITION AND METHODS FOR
TITLE OF INVENTION: IN PLANTS
NUMBER OF SEQUENCES: 1263
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lvor
STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                         GENE EXPRESSION
                                                       US-08-860-038-20
US-08-860-038-21
US-09-580-923-21
US-08-115-497-21
US-08-115-497-21
US-08-291-011-1
US-08-266-065-1
US-08-299-074A-1
  US-09-580-923-9
US-09-580-923-10
5457089-7
                                  US-08-894-511-16
US-08-894-511-17
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US-09-306-042-2
US-09-227-357-81
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                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/679,645
FILING DATE: July 12, 1996
CLASSIPRICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/001,135
FILING DATE: July 13, 1995
APPLICATION NUMBER: 08/300,726
FILING DATE: September 2, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER RADDABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                     APPLICANT: Zwick, Michael G.
APPLICANT: Edington, Brent E.
APPLICANT: McSwiggen, James A.
APPLICANT: Merlo, Patricia Ann Owens
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OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
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; Sequence 25, Application US/08679645
; Patent No. 6350934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219
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TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
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 GENERAL INFORMATION:
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11641.908 Million cell updates/sec
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Sequence 101, Sequence 1, App
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Sequence 5, A
Sequence 1, A
Sequence 12,
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Sequence 23,
Sequence 5,
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                                                                      July 31, 2002, 12:26:33 ; Search time 79.86 Seconds
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-941-445A-4

US-08-742-185-101

US-08-941-445A-6

US-08-941-445A-6

US-09-370-253-23

US-09-370-253-23

US-09-370-253-6

US-08-574-959A-6

US-08-377-014-6

US-08-377-014-6

US-08-357-014-6

US-08-357-014-6

US-08-353-619B-8

US-08-861-12

US-08-861-12

US-08-861-12

US-08-894-511-3

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                                             OM nucleic - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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3785
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Maximum DB seq length: 200000000
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                                                                                                                  Title:
Perfect score:
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APPLICATION NUMBER: US 08/310,429
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 31-UUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08623906A Patent No. 5874217 GENERAL INFORMATION: APPLICANT: Stevenson, Tamara
                                                                                                                                                                            Sequence 101, Application US/08742185; Patent No. 6020476; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: 101:
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                                                                                                                                                                                                                                                                            APPLICANT: Saxena, Richa
APPLICANT: Hawkins, Trevor
APPLICANT: Reeve, Mary Pat
TITLE OF INVENTION: DAL: A GI
NUMBER OF SEQUENCES: 102
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REGISTRATION NUMBER: 32,
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39; Conservative
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-08-623-906A-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                US-08-742-185-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
    Matches
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..2144, 2226..2289, 2413..2513, 2651..2760, 2858
..3101, 3212..3394, 3490..3681, 3793..3879, 3977
..4105, 4227..4343)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.0%; Score 39; DB 3; Length 4800;
100.0%; Pred. No. 6.9e-09;
                                                                                                                                                                  Ouery Match 1.0%; Score 39; DB 4; Length 2267; Best Local Similarity 100.0%; Pred. No. 6.8e-09; Matches 39; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/941,445A
FILING DATE: 30-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,855
FILING DATE: 30-SEP-1996
ATTORNEY AGENT INFORMATION:
ANAWER FASENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Keeling, Peter
APPLICANT: Guan, Hanping
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
CANESPONDENCE ADDRESS:
CADDRESSEE: Greenlee, Winner and Sullivan, P.C.
                                                                                                                                                                                                                                                     3576 cgctacgaccagtacaaggacgcctgggacaccagcgtc 3614
                                                                                                                                                                                                                                                                            Sequence 4, Application US/08941445A Patent No. 6107060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 5370 Manhattan Circle
Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 89-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH: 4800 base pairs
                             LENGTH: 2267 base pairs
TYPE: nucleic acid
STRANDEDMESS: single
TOPOLOGY: linear
US-08-679-645-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
EDNESS: double
GY: not relevant
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                 SEOUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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LOCATION:
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100.0%; Pred. No. 4.4e-05;
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                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/742,185
FILING DATE: 30-0CT-1996
CLASSIFICATION: 435
Query Match
Best Local Similarity 100.0%; Pred. No. 4.4
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LOCATION: 1..28
OTHER INFORMATION: /note= "Nucleotides 1-28 are unique
OTHER INFORMATION: flanking sequence"
APPLICANT: Dvorak, Jan
APPLICANT: Halverson, Joy
TITLE OF INVENTION: Microsatellite Sequences for Canine
TITLE OF INVENTION: Genotyping
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.7%; Score 25; DB 2; Length 252; Best Local Similarity 100.0%; Pred. No. 0.03; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                         ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 104..252
OTHER INFORMATION: /note= "Nucleotides 104-252 are
OTHER INFORMATION: unique flanking sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 29.103
OTHER INFORMATION: /note= "Nucleotides 29-103 are
OTHER INFORMATION: repeat sequence"
                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/623,906A FILING DATE:
CLASSIFICATION: 435
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US-08-941-445A-6
US-08-941-445A-6
Sequence 6, Application US/08941445A
Patent No. 6107060
GENERAL INFORMATION:
APPLICANT: Reeling, Peter
APPLICANT: Guan, Hanping
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J.
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 36,677
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFRAX: 415-398-3249
                                                                                                                                                                                                                                                      ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: DNA (genomic)
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APPLICANT: SCHERMAN, Daniel
APPLICANT: WILS, Pierre
TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION
TITLE OF INVENTION: WITH AN IMMOBILIZED OLIGONUCLEOTIDE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.7%; Score 25; DB 3; Length 2542; Best Local Similarity 100.0%; Pred. No. 0.03; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,445A
FILING DATE: 30-SEP-1997
CLASSIFICATION: 800
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ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                PILING DATE: 30-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,547
REFERENCE/DCCKET NUMBER: 89-97
TELECOMMUNICATION INFORMATION:
TELEPRAX: (303) 499-8080
TELEFXX: (303) 499-8089
TELEFX: (303) 499-8089
TELEFXX: (303) 499-8089
TELEFXX: (303) 499-8089
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Patent No. 6287762
GENERAL INFORMATION:
5370 Manhattan Circle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: cDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2542 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: 453..2282
US-08-941-445A-6
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                                                                                              80303
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                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%; Score 24; DB 4; Length 1865; 100.0%; Pred. No. 0.09; tive 0; Mismatches 0; Indels
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                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Allen, Stephen M.
APPLICANT: Sakai, Hajime
APPLICANT: Thorpe, Catherine J.
TITLE OF INVENTION: Amino Acid Transporters
FILE REFERENCE: BE-1200
                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/370,253
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: 60/097,222
EARLIER FILING DATE: August 20, 1998
NUMBER OF SED ID NOS: 18
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: LAHIVE & COCKFIELD 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: DFN-008 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                      US-09-370-253-5/c; Sequence 5, Application US/09370253; Patent No. 6165792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ 1D NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 3211 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Oryza sativa
US-09-370-253-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      1865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 5
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                                                          RESULT
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APPLICANT: Scherman, Daniel
APPLICANT: Scherman, Daniel
APPLICANT: Wils, Pierre
APPLICANT: Cameron, Beatrice
APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN TITLE OF INVENTION: IMMOBILIZED OLIGONUCLEOTIDE
FILE REFERENCE: 03804,0138-01
CURRENT APPLICATION NUMBER: US/09/580,923
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 08/860,038
PRIOR APPLICATION NUMBER: 09/860,038
PRIOR APPLICATION NUMBER: 1997-06-09
PRIOR APPLICATION NUMBER: 1997-06-09
PRIOR FILING DATE: 1995-11-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.6%; Score 24; DB 4; Length 39;
100.0%; Pred. No. 0.089;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence; OTHER INFORMATION: 01190nucleotide US-09-580-923-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Fred. No. 0.ur
Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                      REGISTRATION NUMBER: 29,699
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: ST94090-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3816
TELEFAX: (610) 454-3808
INFORMATION FOR ESO ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANBONES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2377 aggaagaagaagaagaagaag 2400
                                                                                                                                                            WO FR95/01468
APPLICATION NUMBER: US/08/860,038
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                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/15162
FILING DATE: 16-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 23, Application US/09580923
; Patent No. 6319672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 AGGAAGAAGAAGAAGAAGAAG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                              APPLICATION NUMBER: WO FR FILING DATE: 08-NOV-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                        PRIOR APPLICATION DATA:
                                              CLASSIFICATION: 435
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                                                                                                                     FILING DATE:
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TYPE: nucleic acid
STRANDEDNESS: single
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NAME/KEY: CDS
TOCATION: 439..3847
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                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 02109-1875
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CITY: Boston
STATE: Massach
                            RESULT 11
US-08-574-959A-6
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                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi and Jack L. Strominger TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                               Query Match

O.6%; Score 24; DB 2; Length 3211;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/357,014
FILING DATE: 19-Jul-1999
PRIOR APPLICATION NUMBER: 08/574,959
FILING DATE: CURNOWND-
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISSTRAITON NUMBER: 36.207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.6%; Score 24; DB 4; Length 3211;
100.0%; Pred. No. 0.09;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: DEN-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 439.3157
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-357-014-8
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                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09357014 Patent No. 6291645 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 22
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Best Local Similarity 100.0
Matches 24; Conservative
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                                                      439..3157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
MOLECULE TYPE: CDNA
                                  ; NAME/KEY:
; LOCATION:
US-08-574-959A-8
                                                                                                                                                                                                                                                                                                                         US-09-357-014-8
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TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
AND USES THEREFOR
                                             GENERAL INFORMATION:
APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi
APPLICANT: and Jack L. Strominger
TITLE OF INVENTION: p62 POLYPEPTIDES,
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

O.6%: Score 24; DB 2; Length 3901;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/574,959A
FILING DATE: 19-DEC-95
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-008
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-5941
INFORMATION FOR SEQ ID NO: 6:
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ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Sequence 6, Application US/08574959A
Patent No. 5962224
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COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
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TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                     5394 base pairs
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Best Local Similarity 100.9
Matches 23; Conservative
                                                                                                                                                                                                                                                                                 polyA_signal
4607..4612
                                                                                                                                                                                                                                                                                                                                                                                                                         24; Conservative
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EDNESS: single
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                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                            CAAT_signal
2234..2243
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Best Local Similarity
Matches 24; Conserva
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                                                                                                                                                            NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                    ; LOCATION:
US-08-688-376-1
                                                                                                                                                                                                                                              LOCATION:
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                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                            FEATURE
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TITLE OF INVENTION: NOVEL PROCESS FOR PRODUCING SUBSTANCES
TITLE OF INVENTION: IN MAMMARY GLAND OF TRANSGENIC ANIMAL BY USING MC26 GENE
TITLE OF INVENTION: EXPRESSION-REGULATORY REGION
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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0
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        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/357,014
FILING DATE: 19-Jul-1999
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Floppy disk
COMPUTER: IS Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/688,376
FILING DATE: 30-JUL-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: DILWORTH & BARRESE
4350 LaJolla Village Drive, Suite 300
                                                                                                                                                                                                                             NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REPERENCE/DOCKET NUMBER: DFN-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPAK: (617)227-941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 3901 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COCATION: 439..3847
; SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-09-357-014-6
                                                                                                                                                                 APPLICATION NUMBER: 08/574,959
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Pepper, Frederick W.
REGISTRATION NUMBER: 31,286
REPRENCE/DOCKET NUMBER: 567-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4410
TELEPRAX: 619-453-2839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-688-376-1; Sequence 1, Application US/08688376; Patent No. 6018039
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA
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100.0%; Pred. No. 0.27;
0.6%; Score 24; DB 3; Length 5394;
100.0%; Pred. No. 0.091;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,619B
FILING DATE: December 1, 1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Marcus-Wyner, Lynn
REGISTRATION NUMBER: 34,869
                                                                                                                                                                                                                                                                                                                                                  AUDRESSEE: No. 5919705artis Crop Protection
STREET: 975 California Avenue
CITY: Palo Alto
                                                                                                                                                                                                                         Sequence 8, Application US/08553619B
Patent No. 5919705
GENERAL INFORMATION:
APPLICANT: DeHaan, Petrus T.
TITLE OF INVENTION: Virus Resistant Plants
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Prec. ....
              100.0%; Pred. ...
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/354-3588
TELEFAX: 415/857-1125
INFORMATION FOR SEG ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2621 E.
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July 31, 2002, 10:43:18; Search time 2776.96 Seconds (without alignments) 18396.367 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                    13736207 seqs, 6748477542 residues
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                                                                OM nucleic ~ nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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3785
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	AW448831 AL508333 BL508233 AL508959 AL508959 AL508567 AL508163 BE41430 BE41430 B
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% Query Match Length DB	5513 5624 6538 6538 6538 6538 6538 6538 6538 6538
% Query Match	80444444444444444444444444444444444444
Score	32 52 52 52 52 52 52 52 52 52 52 52 52 52
Result No.	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

Query Match
8.5%; Score 322; DB 9; Length 527;
Best Local Similarity 100.0%; Pred. No. 3.7e-141;
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0; Gaps

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BH122005 AQ740608 BJ163167 BH322444 AZ358393 AZ358393 AZ339932 BB544345	BG075200 BF893280 T44352 BG908116 BF101949 AJ281579 AW596355 T46573	CNSO30NR CNSO32JN CNSO32JN CNSO30JH CNSO59X1 CNSO59X1 CNSO56O CNSO56O CNSO56O CNSO5APL AZ347674	527 bp aestivum o 56 ae, strept ophyta, Li	rriticeae; Triticum. 1 (bases 1 to 527) Clarke, B.C., Hobbs, M. and Appels Genes active in developing wheat Ompublished (2000) Contact: Bryan Clarke Division of Plant Industry C.S. IR.O. C.S. IR.O. The contact of the	au. fiers ticum na" n:4565 "	endosperm" 163 g 7
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179 757 757 514 305 324 166	333 369 459 585 572 572 578 578 578 578 578	907 902 922 968 1020 1050 1062 1101 1101	BRY Triticum aes 1 GI:12019366 at. aet.ivum aestivum ;, Viridiplantae; hyta: Magnolloph	coae; Triticum. 3.C., Hobbs, M. and 2.C., Hobbs, M. and 2.C., hed (2000) Thed (2000) Bryan Clarke Of Plant Industry 10f Plant Canberra, AC. 26246 5054	l 2 6246 5000 bryanc@pi.csiro.au. Location/Qualifie l. 527 /organism="Tritic" /cultivar="Wyuna" /db_xref="taxon:4" /clone="P56-lp" /clone="P56-lp"	ceii_cype= 176 c
		00000000000	AW448831 BRY_1580 BR AW448831 AW448831.1 EST. bread wheat Triticum ae Triticum ae Spermatophy	7 Triticeae, Triticum 1 (bases i to 527) (Clarke, B.C., Hobbs, M. Genes active in devel Unpublished (2000) Contact: Bryan Clarke Division of Plant Ind C.S.I.R.O. GPO Box 1600, Canberr Tel: 61 2 6246 5054	70	115 a
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/note="vector: plasmid pBK-CMV; Site_1: ECORI; Site_2: xhoi; mRNA was made from developing caryopsis (3.-15.DAP) of spring barley variety 'Barke', a high quality malting of spring barley variety 'Barke', a high quality malting variety. Cloning sites: ECORI (5'-end of CDNA) and XhoI (3'-end of CDNA). NOTE: Due to a cloning artefact caused (3'-end of CDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the ECORI site is NOT present, by the kit, in most cases the ECORI site is NOT present, by the ECORI adapter. Average insert size is 1 kb sequence trimming: Vector sequences and sequence ends were trimmed from the 5'-and 3'-end until a 50 bp window contains less than two ambiguities. The maximum length was set to, 700 bp".
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HVSMEh009BD06f Hordeum vulgare 5-45 DAP spike EST library
HVCDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh009BD06f,
                                                                                                                                                                                                                                                                                                                                           Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                           AL508933 Hordeum vulgare Barke developing caryopsis (3.-15.DAP)
Hordeum vulgare cDNA clone HY10D16V 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Institute for Plant Genetics and Crop Plant Research Corrensstr.3, D-06466 Gatersleben, Germany Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de Seg primer: T3 primer for 5'end.
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/lab_host="XLOLR"
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Michalek, W., Weschke, W., Pleissner, K.-P. and Graner, A.
EST sequencing and analysis in barley
Unpublished (2000)
Contact: Michalek W
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Pred. No. 3.3e-13;
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      0; Mismatches
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/db_xref="taxon:4513"
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Varidiplantae; Streptophyta; Poales; Poaceae; Pooideae
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
; Triticeae; Hordeum.
; Triticeae; Hordeum.
; Michalek,W., Weschke,W., Pleissner,K.-P. and Graner,A.

EST sequencing and analysis in barley
Conpublished (2000)

Contact: Michalek W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL506396 ALCHOUM VULGARE BARKE GEVELOPING CARYOPSIS (3.-15.DAP)
HOLGEUM VULGARE CIONE HY02P18T 5', MRNA SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Institute for plant Genetics and Crop Plant Research Corrensstr.3, D-06466 Gatersleben, Germany Email: michalekeipk-gatersleben.de, http://pgrc.ipk-gatersleben.de seq primer: T3 primer for 5'end.
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                                                                                                                                                                                        1.4%; Score 52; DB 9; Length 462; 100.0%; Pred. No. 3.4e-13;
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ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

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EST 04-JAN-2001

linear

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mRNA
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Hordeum vulgare
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California, Riverside (Fenton, SJ Close, TJ Close). Whole California, Riverside (Fenton, SJ Close, TJ Close). Whole Spikes with awns trimmed were collected at 5, 10, 15, 20, 30 and 45 DAP (Fenton). Total RNA was prepared from each pool, equal quantities of all six RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified CNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) CDNA phagemids (Choi)in the TJ Close lab at the University of California, Riverside. Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequence and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been timmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or accourted.
                                                                                                                          Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton, R.D., Close, S.J., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex 5-45 DAP spike cDNA library Unpublished (2001)
On Ang 21, 2000 this sequence version replaced gi:9859804.
Clemson University Genomics Institute
Clemson University Genomics Institute
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                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

    Triticeae; Hordeum.
    Chases 1 to 558)

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this clone see http://www.genome.clemson.edu/orders Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cultivar=_Moream vuigate=_
/db_xref="taxon:4513"
/clone="HVSMEh0098D06f"
/clone_lib="Hordeum vulgare 5-45 DAP spike EST library
HVDNA0009 (5 to 45 DAP)"
/tissue_type="5-45 DAP Spike"
/lab_hsst="SolR"
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Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
209 c 168 g 78 L 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                        100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total hq bases = 215
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence start: 16
High quality sequence stop: 550.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: rwing@clemson.edu
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Matches 52; Conservative
Hordeum vulgare
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BASE COUNT ORIGIN

RESULT AL508959

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source

FEATURES

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sperimatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
; (bases 1 to 700)
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AL506567 Hordeum vulgare cDNA clone HY03121T 5', mRNA sequence.
                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
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                                                                                                                                                                                                                                                                                                            Contact: Michalek W
Institute for Plant Genetics and Crop Plant Research
Corrensstr.3, D-06466 Gatersleben, Germany
Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
Seq primer: T3 primer for 5'end.
Location/Qualifiers
AL508959 Hordeum vulgare Barke developing caryopsis (3.-15.DAP) Hordeum vulgare cDNA clone HY10E20V 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Hordeum vulgare Barke developing caryopsis
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Michalek, W., Weschke, W., Pleissner, K.-P. and Graner, A.
EST sequencing and analysis in barley
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Michalek,W., Weschke,W., Pleissner,K.-P. and Graner,A.
EST sequencing and analysis in barley
Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Hordeum vulgare"
/cultivar="Barke"
/db_xref="taxon:4513"
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Query Match 1.3%; Score 51; DB 10; Length 579; Best Local Similarity 100.0%; Pred. No. 9.7e-13; Matches 51; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                               2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Triticum aestivum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://wheat.pw.usda.gov/genome.
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/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Appels R
Div. of Plant Industry, CSIRO
Canberra ACT 2601 AUSTRALIA
Tel: 61 62 465496
Fax: 61 62 465000
                                                                                                                                                                               213 g
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245 c 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE402419.1 GI:9361887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
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Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence trimming: Vector sequences and sequence ends were trimmed from the 5'-and 3'-end until a 50\ \mathrm{bp} window
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contains less than two ambiguities. The maximum length was
                                                                                                                                                                                                                                                                                                                           /note="Vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2: Xhol; mRNA was made from developing caryopsis (3.-15.DAP) of spring barley variety 'Barke', a high quality malting variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is 1 kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Institute for Plant Genetics and Crop Plant Research Corrensstr.3, D-06466 Gatersleben, Germany Email: michalekeipk-gatersleben.de, http://pgrc.ipk-gatersleben.de Seg primer: 73 primer for 5'end.
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                          Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
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AL508163 Hordeum vulgare Barke developing caryopsis (3.-15.DAP)
Hordeum vulgare cDNA clone HY07P10V 5', mRNA sequence.
                                                                                                                                                                                                                            /clone_lib="Hordeum vulgare Barke developing caryopsis
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/lab_host="XLOLR"
                                                                                                                                                                                                                                                                           tissue_type="developing caryopsis (3.-15.DAP)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 GCGCCATGAACCTCGTCGTCGTCGCCCCGGAGATGGCGCCCTGGAGCAAGAC 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 1.4%; Score 52; DB 9; Length 700; Similarity 100.0%; Pred. No. 3.2e-13; 52; Conservative 0; Mismatches 0; Indels
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Corrensstr.3, D-06466 Gatersleben, Germany
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                                                                                                                           /organism="Hordeum vulgare"
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                                                 Seq primer: T3 primer for 5'end.
Location/Qualifiers
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                                                                                                                                                   /cultivar="Barke'
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229 c 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52; Conservative
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                                                                                                         source
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(3'-end of CDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is I kb Sequence trimming: Vector sequences and sequence ends were trimmed from the 5'-and 3'-end until a 50 bp window contains less than two ambiguities. The maximum length was
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
1 (bases 1 to 579)
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Location/Qualifiers
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Best Local Similarity
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,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
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Mammalia; Eutheria; Rodentía; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 421)
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100.0%; Pred. No. 9.6e-13;
tive 0; Mismatches 0; Indels
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/note="Vector: Bluescript II SK(-)"
215 c 201 g 86 t 12 others
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International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
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/clone="SCU008.C04"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.

1 (bases I to 494)

Clark, B.C., Hobbs, M. and Appels, R. Genes active in developing wheat endosperm

Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
Brain genomic DNA was isolated and partially digested
with a combination of ECORI and ECORI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
BLOB electrocompetent cells (BRL Life Technologies). "
134 c 24 g 248 t
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                                                                                                                                                                                                                                                                                 Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 447 row: D column: 2
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and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other Casss: RPCI-23-447D2.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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100.0%; Pred. No. 2.1e-09,
tive 0; Mismatches 0)
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Tel: 61 2 6246 5054
Fax: 61 2 6246 5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="RPCI-23-447D2"
/clone_lib="RPCI-23"
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Division of Plant Industry
C.S.I.R.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: bryanc@pi.csiro.au
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW448811.1 GI:12019346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: SP6
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AZ733073 165 bp DNA linear GSS 25-JAN-2001
RPCI-24-118F9.TV RPCI-24 Mus musculus genomic clone RPCI-24-118F9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS 04-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 118 row: F column: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_type="Spleen/Brain"
/note="Vector: pTaRBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 165)
Zhao,S., Nietman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
Russell,D., de Jong,P. and Praser,C.M.
                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                                                                                    Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Tel: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse BAC End Sequences from Library RPCI-24 Unpublished (1999)
Other_GSSs: RPCI-24-118F9.TJ
244 GCGTCACCGACAGATTCCGGCGTCCAGGTTTTCAGGGCCT 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.0%; Score 37; DB 12; I. 100.0%; Pred. No. 5.3e-06; itive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2379 gaagaagaagaagaagaagaagaagaagaagaag 2415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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/clone="RPCI-24-118F9"
/clone_lib="RPCI-24"
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                                                                                                                                                                                                                                   AZ733073.1 GI:12496755
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AZ462781.1 GI:10620906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 301 838 0208
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                                                                                                                                                                                     DNA sequence.
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nes 37; Conserva
                                                                                                                                                                                                                                                                                 house mouse.
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                                                                                           RESULT 13
                                                                                                                    AZ733073/c
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                          q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BM368238 444 bp mRNA linear EST 10-JAN-200
EBed01_SQ002_J02_R IGF Barley EBed01 library Hordeum vulgare cDNA
clone EBed01_SQ002_J02 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Triticeae; Hordeum.
1 (bases 1 to 444)
Heddey, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L.,
Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.
Development of Barley Transcriptome Resources
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: rwaugh@scri.sari.ac.uk
All sequence has a Phred quality score of 20 or over
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.1%; Score 40; DB 10; Length 444;
                                                                                                                                                                                                                                                         Length 494;
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/clone-lib-"IGF Barley EBed01 library"
/tissue_type="Endosperm"
/dev_stage="6 days post anthesis"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                3322 ccggcggtgcctctccatggtggtgcgcgccacgggcagcg 3362
                                                                                                                                                                                                                                                                                                                                                                   3189 gcgtcaccgacagattccggcgtccaggttttcagggcct 3228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Invergowrie, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
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                                                                                                                                                                                                                                                      Score 41; DB 9; L
Pred. No. 5.5e-08;
                     /organism="Triticum aestivum"
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/cultivar="Optic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pred. .v.
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Unit of Genomics
Scottish Crop Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene Function) project.
                                                                                                                                /cell_type="endosperm"
170 c 160 a
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                                                            /db_xref="taxon:4565"
                                                                                                                                                          160 g
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                                                                                                            /clone_lib="BRY"
                                         /cultivar="Wyuna'
                                                                                         /clone="P51-2A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BM368238.1 GI:18111628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: M13 reverse
                                                                                                                                                                                                                                                                         Best Local Similarity 100.0
Matches 41; Conservative
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source
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house mouse.
                                                            Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114 [pb]ARL29072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ368386 380 bp DNA linear GSS 02-OCT-2000 LM0118M19F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0118M19 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                        Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)
Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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/db_zerf="caron:10090"
/clone="uUGC1M0271G17"
/clone="lub="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PW042nv; Purified genomic DNA from M.
musculus C57BL/63 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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100.0%; Pred. No. 4.9e-06;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               rel: 801 585 5606
Fax: 801 585 7177
Frail: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 260.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: plasmid ends
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Best Local Similarity 100.C
Matches 37; Conservative
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                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
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DEFINITION
                        ORGANISM
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ORIGIN
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                                                                                                         REFERENCE
                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                        TITLE
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                                                                                                                                                                                                                                                                                                                     COMMENT
SOURCE
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymerlectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114 gblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Rodentia, Sciurognathi; Murinae; Musinae; Musinaes; Lto 380)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/G1(male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                           Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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1.0%; Score 37; DB 12; I
Best Local Similarity 100.0%; Pred. No. 4.5e-06;
Matches 37; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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/organism="Mus musculus"
/strain="057BL/60"
/db_xref="taxon:1000"
/clone="UUGCIM0118M19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plate: 0118 row: M column: 19
Seg primer: CGTTGTAAAACGACGGCCAGT
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High quality sequence stop: 380.
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Job time: 15085 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

July 31, 2002, 14:02:43; Search time 389.91 Seconds

(without alignments) 16666.721 Million cell updates/sec

1 gtttggtttcgctgtttttc.....tggaccgcgtgttcgtcgac 3785 US-09-899-718A-1 Perfect score: Sequence: Title:

Searched:

OLIGO_NUC Gapop 60.0 , Gapext 60.0 Scoring table:

1736436 seqs, 858457221 residues Word size :

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

3472872

Post-processing: Listing first 45 summaries

Database:

N_Geneseq_032802:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

		Description	TOTO AT TOO A		HUMBAN OKEY OKET24	DNA seguence of th	Crapulo bound atten	granute nound star	Zea mays waxy dene	Human foots 1	יומווימיו דחברמד דדי הב	Probe #13741 for q	Hilman bond memin	MOTTE III TOTION	Probe #13097 for q	DNA encoding novel
SUMMARIES		ΙD		AAC74569	000000000000000000000000000000000000000	STCOOPUL	AAX63355	AAV20752	70/07/00	ABA68266	ADASESSE	C/7CC494	AAK42405	ANTOSTER	#0TC7TUG	AAS71148
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		re Match Length DB ID		333	1915	1 1	2267	4800		9/7	276	1 6	7/6	276		460
æ	Query	Match		1.0	1.0		1.0	1.0	,	٦.	0.[o . †	0		7.0
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23 AAS69548	AAS9069	AAS754	AAS907	21 AA292583	AAC498	AAC398	-	AAC5508				AAS6811				21 AAC52482		AAC4417	AAC401	AAF2229	AAC1304		AAT6506	AAX1780			ABA253			21 AAC49195	AAC3	AAC3616	AAC4331	AA045	AAS8669
508	7 5	÷ :	7.11	35	60		7.1	ຽ	7											584												9/9	265		340
1.0																												0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7
37	7 0	, ,	3.1	31	29	29	29	29	28	27	27	27	27	27	27	56	26	56	26	26	25	25	25	25	22	22	25	25	25	25	25	22	25	25	25
10	17	7 T	CT.	74	15	16	17	18	19	20	21	22	23	24	25	56	c 27	28	53	30	31	c 35								40	41	c 42		44	45

ALIGNMENTS

AAC74569 standard; cDNA; 333 BP. (first entry) 08-FEB-2001 AAC74569

Human ORFX ORF124 polynucleotide sequence SEQ ID NO:247.

Whuman; open reading frame; ORFX; detection; cytostatic; hepatotropic; wulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; antibronian; nootropic; neuroprotective; antibroniant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coaquiant; vasotropic; antidiabetic; whypotensive; dermatological; immunosuppressive; antiinflammatory; antibraterial; antibacterial; antifungal; antirheumatic; antithyroid; wantianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; araft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; school ester Storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; thrombosis; contraceptive; ss.

Homo sapiens.

WO200058473-A2.

05-OCT-2000.

31-MAR-2000; 2000WO-US08621.

DNA encoding novel

98WO-US06660.

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Merlo PAO,
03-APR-1998;
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    ŏ
                                                                                                                                                                                                                                                                                                                                                                          AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; cartiportici antiporvulsant; antiarthritic; immunosuppressant; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressant; cartiportantary; and antianeamic. The sequences can be used for determining antithyroid; and antianaemic. The sequences can be used for determining antithyroid; and antianaemic. The sequences can be used for determining antithyroid; and antianaemic. The sequences can be used for determining correct and conditions associated with an ORFX-associated disorder. The preparative disorders, neurodegenerative disorder. The nucleic acids can be used to express ORFX proteins in gene therapy corrects. The proteins and nucleic acids may be used to treat cancers, crectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, enclodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, papertension, hypothyroidsm, cholesterol ester storage, systemic lupus crythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Non-glycogen-like polysaccharide production; fermentation; waxy gene; starch synthesis enzyme; glycogen-synthesis enzyme; glycogen synthesis; non-starch branching gene; amylopectin; amylose; plant-like starch; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                  Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 1.0%; Score 39; DB 21; Length 333; Local Similarity 100.0%; Pred. No. 3.3e-08; nes 39; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 333 BP; 78 A; 96 C; 100 G; 59 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA sequence of the maize waxy gene.
                                                                                                                                                                                                                                                                                                                                                     Claim 5; Page 560; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX60319 standard; DNA; 1915 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                 31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                                                                                                               Shimkets RA, Leach M;
                                                                                                                                       (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                    WPI; 2000-602362/57.
                                                                                                                                                                                                                                         P-PSDB; AAB40360
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The specification describes a method for the production of non-glycogen-like polysaccharides in a host. The method comprises transforming a host, suitable for fermentation, with genes encoding starch- or glycogen-synthesis enzymes, and fermenting the transformants. The specification also describes hosts transformed with a gene active in glycogen synthesis and at least one non-starch branching gene, involved in production of amylopectin or amylose in its original host. The method is used to produce plant-like starches by fermentation and new starches in plants. These starches are useful for all food and non-food applications of starch. The present sequence is used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maize; corn; Zea mays; delta-9 desaturase; GBSS; target; substrate; granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme; modulation; gene expression; transgenic plant; cleavage; canola plant; caffeine synthesis; coffee plant; nicotine production; tobacco; fruit ripening; flower pigmentation; lignin production; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                             producing non-glycogen-like polysaccharides in bacteria, fungi or plants - transformed with genes for enzymes involved in starch or glycogen synthesis allows fermentative production of starches with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
1.0%; Score 39; DB 19; Length 1915;
Best Local Similarity 100.0%; Pred. No. 3.3e-08;
Matches 39; Conservative 0; Mismatches 0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1915 BP; 365 A; 610 C; 641 G; 299 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3576 egetaegaecagtaeaaggaegeetgggaeaceegegte 3614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        355 egetacegetacaaggacectegggacaccagegte 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zwick MG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Granule bound starch synthase encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ), Guo L,
Young SA,
                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 49; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX63355 standard; cDNA; 2267 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-US11689.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the course of the invention.
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                                                           (EXSE-) EXSEED GENETICS LLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Folkerts O,
Skokut TA, Yo
97US-0042939
                                                                                                                                                                                                                                                                                                                                                                             engineered properties
                                                                                                                             Guan H, Keeling PL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOWC ) DOWELANCO.
                                                                                                                                                                                        WPI; 1998-568285/48.
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   04-APR-1997;
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/number= 6
2290..2412
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1554..1684
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887..900
/*tag= 1
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2145..2225
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/number= 6
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/*tag= bb
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/*tag= cc
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/number= 9
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867..873
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/number= 9
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                                                                         The present invention describes an enzymatic nucleic acid molecule (I) with RNA cleaving activity, which modulates the expression of a plant gene. Also described is a gene comprising a cDNA sequence encoding maize Delta-9 desaturase. (I) can be used to modulate expression of a gene, preferably Delta-9 desaturase or a granule bound starch synthase (GBSS) gene, in a plant (preferably a maize or canola plant, icotine production in a tobacco plant, fruit ripening processes in an apple, tomato, pear, plum or peach plant, flower pigmentation in a rose, petunia, chrysanthemum or marigold plant or lignin production in a tobacco, aspen, poplar or pine plant.
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/note= "GC stretch, potential regulatory factor binding"
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/note= "GC stretch, potential regulatory factor binding"
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/note= "GC stretch, potential regulatory factor binding'
                                                                                                                                                                                                                                  Gaps
                         Ribozyme which modulates plant gene expression - preferably modulates expression of DELTA-9 desaturase or granule bound starch synthase in maize or canola
                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                Length 2267;
                                                                                                                                                                                                           1.0%; Score 39; DB 18; Length 22, 100.0%; Pred. No. 3.3e-08; tive 0; Mismatches 0; Indels
                                                                                                                                                                                 Sequence 2267 BP; 465 A; 699 C; 733 G; 370 T; 0 other;
                                                                                                                                                                                                                                             SER; starch-encapsulating region; fusion vector; glucosyl transferase; ss.
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/note= "direct repeat 1"
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/note= "direct repeat 1"
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/note= "direct repeat 1"
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/note= "direct repeat 1"
                                                           Example 9; Page 31-33; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
283..287
                                                                                                                                                                                                                                                                                                         AAV29752 standard; DNA; 4800 BP.
                                                                                                                                                                                                         Query Match
Best Local Similarity 100.C
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                            11-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             .292
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         WPI; 1997-202224/18.
                                                                                                                                                                                                                                                                                                                                                               Zea mays waxy gene.
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                                                                                                                                                                                                                                                                                                                                                                                                         Zea mays.
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AAV29752
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'note= "GC stretch, potential regulatory factor"
/*tag= i
/note= "target duplication site (Ac7)"
                                                                                                                                                                                                        /*tag= m
/note= "transcriptional start site"
1449..4343
                                                                                                                                                                                                                                                                   /*tag= n
/product= glucosyl transferase
//forte= "contains introns"
901..1080
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Length 4800;

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The sequence is that of the waxy gene which codes for glucosyl transferase. It can be used in the production of a hybrid polypeptide comprising a starch-encapsulating region (SER) fused to a payload protein. The hybrid polypeptide can be used to make modified starches comprising the payload protein, selected from,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e.g. hormones, growth factors, antibodies, enzymes, dyes, immunoglobulins, etc. The modified starch can also be used to provide grain feeds enriched in amino acids. By encapsulating the payload protein in starch, it is more resistant to degradation by stomach acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hybrid polypeptide comprising starch-encapsulating region and protein - useful for, e.g. producing protein(s) resistant to degradation by stomach acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4800 BP; 935 A; 1414 C; 1446 G; 1005 T; 0 other;
                                                                                                         /*tag= kk
/note= "target duplication site (Spm 18)"
                   /*tag= hh
/note= "target duplication site (Ac9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 29-31; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EXSE-) EXSEED GENETICS LLC.
                                                                                                                                                                                                                                                                                                                                                                                                                          97WO-US17555.
                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-0026855.
                                                                                                                                                                                                             /number= 12
3977..4105
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4570..4575
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3880..3976
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3793..3879
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'number= 10
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        3358..3489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guan H, Keeling P;
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                                                                                                                                                                                                                                                                                                                                   polyA_signal
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                                                                                                                                                                                                                                                                                      Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
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Probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pott_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; SEQ ID NO 16571; 639pp + sequence listing; English.
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100.0%; Pred. No. 3e-07;
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                           0; Indels
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1.0%; Score 39; DB 19; 1
100.0%; Pred. No. 3.3e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity 100.0%; Pred. No. 3e-37; Conservative 0; Mismatches
 Query Match
Best Local Similarity 100.0%; Pred. No. 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanzel DK, Chen W, Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
                                                                                                                                                                       ABA68266 standard; DNA; 276 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                     01-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                            WO200157277-A2
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                                                                                                                                                                                                        ABA68266;
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                                                                                                                                                             ABA68266/c
                                                                                                                                               RESULT
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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe #13097 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of single exon nucleic acid
Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; SEQ ID NO: 16962; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 276;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 276 BP; 23 A; 81 C; 20 G; 152 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.0%; Score 37; DB 22; Le
100.0%; Pred. No. 3e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 GAAGAAGAAGAAGAAGAAGCAGAAGAAGAAGAAG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. No. 3e-
                                                                                                                                                                                                                                                                                                                                                                                        Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAI23164 standard; DNA; 276 BP
                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                  2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
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                                                                                                                                                                30-JAN-2001; 2001WO-US00668
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Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488900/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cervical cancer; ss
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                                                                                        WO200157276-A2
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                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                               27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                      26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                          03-AUG-2000;
21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAI23164;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single exon nucleic acid probes for analyzing gene expression in human
                                                                                        for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                       Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human bone marrow expressed single exon probe SEQ ID NO: 16962.
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Pred. No. 3e-07;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 276 BP; 23 A; 81 C; 20 G; 152 T; 0 other;
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100.0%; Pred. No. 3e-(
+ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0632366.
2000US-0234687.
2000US-0236359.
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2000US-0608408
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                                                      (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                       WO200157274-A2.
                                                                                        Probe #13741
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27-SEP-2000;
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                 ABA35275;
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                                                                                                                                                                                           (SENP). The present sequence is one such probe. The SENPS are derived from human Hela cells. The SENPS can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                   The present invention relates to human single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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0
                                                                                                                           Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                      analyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                               1.0%; Score 37; DB 22; Length 276;
                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                               Sequence 276 BP; 23 A; 81 C; 20 G; 152 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding novel human diagnostic protein #6952.
                                                                                                                                                                                                                                                                                                                                                                                             2379 gaagaagaagaagaagaagaagcagaagaagaagaag 2415
                                                                                                                                                                                                                                                                                                                                                                                                           243 GAAGAAGAAGAAGAAGAAGAAGCAGAAGAAGAAGAAG 207
                                                                                                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. NO. 35.
                                                                                                                                                             Claim 25; SEQ ID No 13097; 487pp; English.
                                                                             Penn SG, Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS71148 standard; cDNA; 460 BP.
                                                       (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2001; 2001WO-US08631.
2000US-0632366.
          2000US-0234687.
2000US-0236359.
                                04-OCT-2000; 2000GB-0024263.
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                                                                                                   WPI; 2001-488901/53.
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03-AUG-2000;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypetide and polynuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AASA(197-AASA(546 represent novel human diagnostic coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 460 BP; 209 A; 51 C; 128 G; 72 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences.
Claim 1; SEQ ID No 6952; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-2001; 2001WO-US08631.
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Claim 1; SEQ ID No 26501; 103pp; English.
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                                                                                                                                                                                                                                                      and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPPO
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             Claim 1; SEQ ID No 5352; 103pp; English.
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23-AUG-2000; 2000US-0649167.
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P-PSDB; ABG26510.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in disorders for gene mapping, identification of mutations are responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and also are applications and a sequences. AAS64197-AAS9464 represent novel human
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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3e-07;
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Matches
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in the polynucleotide and polynucleotide sequences have applications in the polynucleotide sequences and the polynucleotide sequences have applications in the polynucleotide sequences have applications in the polynucleotide sequences have applicated and polynucleotide sequences h
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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100.0%; Pred. No. 3e-07;
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polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, and properties chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The conformal activity of (II) is useful in gene therapy techniques for identifying expressed genes. (I) is useful in gene therapy techniques for restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in dispnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and no produce other types of data and products dependent on DNA and and application of mine acid sequences. Abs6197-AAS9564 represent novel human
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Note: The sequence data for this patent did not appear in the printed
specification, but was obtained in electronic format directly from WIPO
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100.0%; Pred. No. 0.00023;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saxena R, Page DC, Reijo R;
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present in interval 6D and/or 6E of the distal portion of Yq, mutations in which are associated with reduced sperm count. The DAZH gene (AAZ92580) is located on chromosome 3; however, the entire DAZ gene family, including DAZH is expressed in germ cells. DAZ and DAZH nucleotide sequences may be used as a source of primers and probes for the diagnosis of reduced sperm count associated with alteration or deletion of the DAZ gene. They are also used as human chromosome Y markers. Functional DAZ genes can be used in gene therapy for treating
                                                                                                        reduced sperm counts. Sequence AA292499 represents human DAZ CDNA, and sequences AAZ92583-292584 are genomic DAZ sequences. Sequences AAZ92491-292492 are partial DNA sequences of DAZ gene family members.
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                                                                                                                                                                                                  Query Match 0.8%; Score 31; DB 21; Length 43795; Best Local Similarity 100.0%; Pred. No. 0.00023; Matches 31; Conservative 0; Mismatches 0; Indels 0
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Page 10

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Listing first 45 summaries
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18
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.		000 9086	1122 1122 1132 1143	10000	C 23 C 24 C 25 C 25 C 26

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ALIGNMENTS

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Patent No. 6124116
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
ITLE OF INVENTION: NOVEL RAB PROTEINS
ITLE OF ENVENTION: NOVEL RAB PROTEINS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                       ADDRESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PF-0139 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/741,411
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SOFTWARE: FASTEGO VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/741,41
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 890 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 415-855-055
TELEFAX: 415-845-4166
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Query Match

80.0%; Score 14.4; DB 3; Length 890;

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                                                                          ADDRESSEE:
                                                                                                                                                                            10022
                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-147-592A-1
                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                Gaps
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                                                                                                                                                                                                                                                                   APPLICANT: Huss-Peter; Knapp Stefan; Brust, Stefan;
APPLICANT: Griler, Lutz G.; Eberle, Josef; Kaptue, Lazare;
APPLICANT: Zekeng, L opold Achengui
TITLE OF INVENTION: Retrovirus From The HIV Group And Its Use
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hauser, Hans-Peter; Knapp Stefan; Brust, Stefan; APPLICANT: G rtler, Lutz G.; Eberle, Josef; Kaptue, Lazare; APPLICANT: Zekeng, L opold Achengui TITLE OF INVENTION: Retrovirus From The HIV Group And Its Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 80.0%; Score 14.4; DB 1; Length 1070; Best Local Similarity 93.8%; Pred. No. 48;
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                              1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
93.8%; Preu. ....
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FILING DATE: 16-FEBRUARY-1996
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 05 262
FILING DATE: 16-FEBRGARY 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Hanson, No. 5798205man D. REGISTRATION NUMBER: 30,946 REFERENCE/DOCKET NUMBER: LEDER 2 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                        Sequence 11, Application US/08602713
Patent No. 5798205
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 11, Application US/08989493
; Patent No. 6162631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212) 688-9200
TELEFRA: (212) 838-3884
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Felfe & Lynch STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1070 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                             282 ATACTCGGGTCATGTT 267
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                          15; Conservative
                                                                   1 atactctggtcatgtt 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York City
New York
        Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10022
                                                                                                                                                                                           US-08-602-713-11
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Gaps
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                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: Pd-ease #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Opioid Receptor Genes,
Compositions and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Hanson, NC. CLEER SERVING NUMBER: LEDER 203
REGISTRATION NUMBER: LEDER 203
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 838-3884
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1070 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 16-FEBRGARY-1996
APPLICATION NUMBER: DE 195 05 262
FILING DATE: 16-FEBRUARY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/989,493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    United States of America
TITLE OF INVENTION: (MVP-2901/94)
                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1, Application US/08147592A
; Patent No. 6096513
                                                               E: Felfe & Lynch
805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: Genomic DNA US-08-989-493-11
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APPLICANT: Reisine, Terry
APPLICANT: Yasuda, Kazuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      403 ATACTCTTGTCATGTT 418
                                                                                                                                                                                                                                                                                          SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 atactctggtcatgtt 16
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STREET: P.O. Box 4433
CITY: Houston
                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                         New York City
New York
                                                                                                                                                                                                                                           IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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APPLICANT: ALTAGOUT, M. AMIN
TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
TITLE OF INVENTION: RESPONSES WITH BETAZ INTEGRINS
TITLE OF INVENTION: RESPONSES: 53
CORRESPONDENCE: 53
ADDRESSE: ADDRESS:
ADDRESSE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CIIY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.0%; Score 14.4; DB 4; Length 1410; 93.8%; Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OMPERATURE: SYSTEM: Windows95
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/476,062A
FILING DATE: 07-JUN 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,081
                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: MARK B. WILSON
RECISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:140/WIM
TELEPHONE: (512) 418-3000
TELEPHONE: (513) 789-2679
TELER: 79-0924
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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FILING DATE: 28-JUN-1988
ATJORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00786/068003
APPLICATION NUMBER: 08/147,592
FILING DATE: 5 No. 6319686ember 1993
CLASSIFICATION: 435
                     20 May 1994
1817 435
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APPLICATION NUMBER: 07/212 677
FILING DAMP
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US-08-476-062A-40/c
; Sequence 40, Application US/08476062A
; Patent No. 5877275
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APPLICATION NUMBER: 07/637,830
FILING DATE: 04-JAN-1991
APPLICATION NUMBER: 07/539,842
APPLICATION NUMBER: 07/539,842
                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 80.0°
Best Local Similarity 93.8°
Matches 15; Conservative
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EDNESS: single
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LOCATION: 186..1325
                                                             APPLICATION NUMBER:
FILING DATE: 20 May
CLASSIFICATION: 435
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ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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Patent No. 6319686
GENERAL IPPORANTION:
APPLICANT: BELL, GRAEME
APPLICANT: REISINE, TERRY
APPLICANT: YASUNA, KAZUKI
TITLE OF INVENTION: OPIOID RECEPTORS: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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93.8%; Pred. No. 50;
tive 0; Mismatches
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          APPLICATION NUMBER: US/08/147,592A FILING DATE: 05-NOV-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Arnold, White & Durkee STREET: P. O. Box 4433
                                                                                                                                                                                                                                                                                ARCD: 105
                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,694
FILING DATE: 30-JUL-1993
CLASSIFICATION: 435
APPLICATION NUMBER: 08/066,296
FILING DATE: 20-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
APPLICATION NUMBER: 08/100,694
FILING DATE: 30 July, 1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                         NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFRENCE/DOCKET NUMBER: ARCD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                 TELEX: N/A
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415 ATTCTCTGGTCATGTT 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 93.8
Matches 15; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: 186..1325
US-08-147-592A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Houston
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STATE: Texas
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US-08-292-694A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Frudakis, Tony N.
Smith, John M.
Read, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                              APPLICANT: ARNAOUT, M. AMIN
TITLE OF INVENTION: HUMAN CR3a/b HETERODIMERS
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/78,871
FILLING DATE: 16-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 210121.419C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,789A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Potter, Jane E. R. REGISTRATION NUMBER: 33,332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 204, Application US/08991789A; Patent No. 6225054; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 11-Dec-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 248 base pairs
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 539,842
FILING DATE: 18-JUN-1990
APPLICATION NUMBER: 22,573
FILING DATE: 28-JUN-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 204:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                  1258 ACTCTGGTCATGTTGA 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 1258 ACTCTGGTCATGTTGA 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 93.8 Matches 15; Conservative
                            3 actctggtcatgttaa 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 actctggtcatgttaa 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO:1:
; LENGTH: 3533
                                                                                                                                                                            ; Patent No. 5424399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-08-991-789A-204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                      5424399-1/c
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                            δλ
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0
                                                                                                                                                                                                                                                                                                                                                              80.0%; Score 14.4; DB 2; Length 3533; 93.8%; Pred. No. 56; tive 0; Mismatches 1; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-0596-01314-40/c

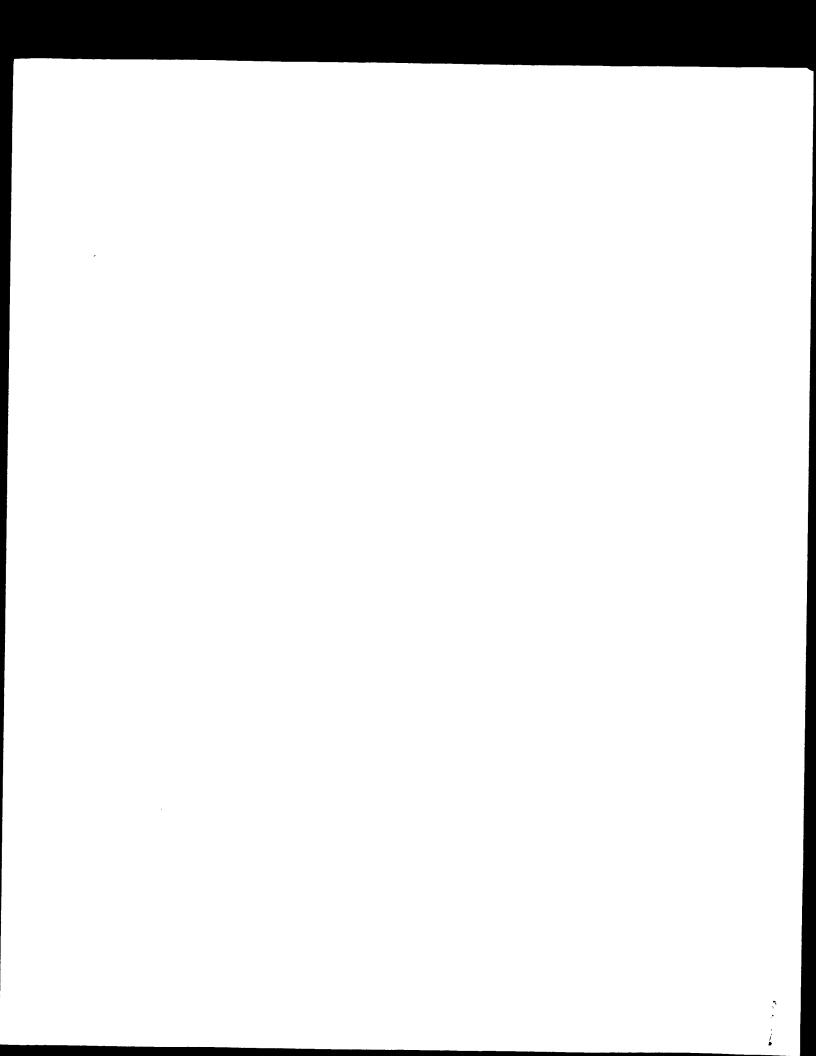
Sequence 40, Application PC/TUS9601314
GENERAL INFORMATION:
APPLICANT M. Amin Arnaout
ITILE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
TITLE OF INVENTION: ANTAGONISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PS/2 MAGEL 502 Or 558X
OPERATING SYSTEM; MS-DOS (Version 5.0)
SOFTWARE: WORDPETFECT (Version 5.1)
CURRENT APPLICATION NUMBER: PCT/US96/01314
PILICED DATE: 30-JAN-96
PRIOR APPLICATION NUMBER: 08/380,167
FILING DATE: 30-JAN-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.8%; Pred. No. 56;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     00786/267001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: John W. Freeman
REGISTRATION NUMBER: 29,066
                                                         TELEX: 200154
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 3533 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 20154
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 3533 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                               NAME/KEY: Coding Sequence LOCATION: 75...3530
                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                         Query Match 80.03
Best Local Similarity 93.83
Matches 15, Conservative
                   TELEPHONE: 617/542-507
TELEFAX: 617/542-8906
                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 93.8 Matches 15; Conservative
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EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                             US-08-476-062A-40
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STREET: 620 Newport
CITY: Newport Beach
STATE: CA
COUNTRY: USA
FILE REFERENCE: 53679
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SEQ ID NO 12
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                                                                                                                                   TYPE: DNA
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APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                       Gaps
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GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
NUMBER OF SEQUENCES: 297
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.7%; Score 13.8; DB 4; Length 248; 88.2%; Pred. No. 83; tive 0; Mismatches 2; Indels
                                                                                               76.7%; Score 13.8; DB 4; Length 248; 88.2%; Pred. No. 83;
tive 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FITTER: US/09/062 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                   ; SEQUENCE DESCRIPTION: SEQ ID NO: 204: US-08-991-789A-204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 210121.419C2 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UMBER: US/09/062,451
04-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                         Sequence 204, Application US/09062451 Patent No. 6344550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 204:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 88.2'
Matches 15; Conservative
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                                                                                                                                                                             1 atactctggtcatgtta 17
           TOPOLOGY: linear
                                                                                                     Query Match 76.73
Best Local Similarity 88.23
Matches 15; Conservative
                                                                                                                                                                                                                 71 ATGCTCTGATCATGTTA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington
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US-09-062-451-204
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ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 0.
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US-09-457-046B-15
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                                                                                                                                                                                                                                                                                             US-09-062-451-204
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APPLICANT: Julian Gordon
APPLICANT: Steven C. Hodges
APPLICANT: Steven R. Klass
APPLICANT: Michael R. Klass
APPLICANT: Jon D. Kratchvil
APPLICANT: Stephen D. Stroupe
APPLICANT: Stephen D. Stroupe
TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the Urin
TITLE OF INVENTION: Tract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Pastan, Ira APPLICANT: Pastan, Ulrich APPLICANT: Brinkmann, Ulrich TITLE OF INVENTION: CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN (CSP) AND AN NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.7%; Score 13.8; DB 4; Length 3147; 88.2%; Pred. No. 1.2e+02; Live 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                DB 4; Length 908;
                                                                                                                                                                                                                                                                                                               2; Indels
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620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                Score 13.8; DB:
Pred. No. 99;
0; Mismatches
CURRENT APPLICATION NUMBER: US/09/457,046B CURRENT FILING DATE: 1999-12-07 NUMBER OF SEQ ID NOS: 74 SOFTWARE: Patentin Ver. 2.1 SSQ ID NO 15 LENGTH: 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/153,804
CURRENT FILING DATE: 1998-09-15
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08480662 Patent No. 5759782 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 12, Application US/09153804
; Patent No. 6207380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Patricia Billing-Medel
                                                                                                                                                                                                                                                                     76.7%;
88.2%;
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APPLICANT: Paula N. Friedman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 tactctggtcatgttaa 18
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                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.2's
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                              1 atactctggtcatgtta 17
                                                                                                                                                                       , ORGANISM: Taxus cuspidata US-09-457-046B-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 15; Conserva
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76.7%; Score 13.8; DB 3; Length 3180; 88.2%; Pred. No. 1.2e+02; tive 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAL INFORMATION.
APPLICANT: Pastan, Ira
Brinkmann, Ulrich
TITLE OF INVENTION: CELLULAR APOPTOSIS SUSCEPTIBILITY
PROTEIN (CSP) AND ANTISENSE CSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPERENCE/DOCKET NUMBER: NIH112.001A
TELECOMNNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
FILING DATE: 20-Jan-1999
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
               NAME: Israelsen, Ned A
REGISTRATION NUMBER: 29,655
REFENCE/DOCKET NUMBER: NIH112.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/918,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Israelsen, Ned A
REGISTRATION NUMBER: 29,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 1, Application US/09234232
; Patent No. 6232086
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 3180 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
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    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 1336 TTCTCTGGTTATGTTAA 1352
                                                                                                                                                                                                       LENGTH: 3180 base pairs
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                                                                                                      TELEPHONE: 619-235-855
TELEFAX: 619-235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Conservative
                                                                                                                                                                                                                               nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: <Unknown>
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                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: CA
                                                                                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                                                                                                                                    ; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-918-190-1
                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO
                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
                                                                                                                                                                                                                                                                      POPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-09-234-232-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.7%; Score 13.8; DB 1; Length 3180; 88.2%; Pred. No. 1.2e+02; Live 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Brinkmann, Ulrich
APPLICANT: Brinkmann, Ulrich
APPLICANT: BLINKMANION: CELLULAR APOPTOSIS SUSCEPTIBILITY
TITLE OF INVENTION: PROTEIN (CSP) AND ANTISENSE CSP
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,662
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: NIH112.001A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/918,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08918190
Patent No. 6072031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
                                                                                                                                                                                                                                                                                                  29,655
                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 3180 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 1336 Trefedenargina 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                           NAME: Israelsen, Ned A
REGISTRATION NUMBER: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 88.23
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 tactctggtcatgttaa 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-480-662-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: lir
MOLECULE TYPE:
                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-918-190-1
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0



GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

July 31, 2002, 12:12:12; Search time 5855.71 Seconds (without alignments) 41.489 Million cell updates/sec Run on:

US-09-899-718A-8 18 Perfect score:

1 atactctggtcatgttaa 18 Sedneuce:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

13736207 seqs, 6748477542 residues Searched:

27472414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST:* Database :

em_estba:*
em_esthum:*
em_estin:*
em_estin:*
em_estov:*
em_estpi:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ю				
Result No.	t Score		Query Match Length DB	DB	ID	Description
	1 17	4. 46	1441	101	BG531376	BG531376 602559625
)	7 16 4	91	344	10	BF516695	BF516695 NXSI_002_
	16.4	91.1	513	10	BG318395	BG318395 NXPV_013_
c	4 16.4	91.1	558	12	A0621441	AQ621441 HS_3019_B
)	16.4	91.1	564	12	AZ144687	AZ144687 SP_0041_B
	16.4	91.1	571	10	BG318023	BG318023 NXPV_008_
Ç	7 16.4	91.1		12	AZ207084	AZ207084 SP_0127_A
)	16	88.9		12	AQ150695	AQ150695 HS_3203_A
c	91	88.9		σ	AW812504	AW812504 CM4-ST018
ۍ د	15.6	86.7		12	CNS02T50	AL212759 Tetraodon
) (15.4			10	BI287040	BI287040 UI-R-CT0s
, -	15.4		225	σ	BE142340	BE142340 CM3-HT014
,-	15.4	25.00	297	6	BB024447	BB024447 BB024447
, ר	15.4	· a.	303	6	BB289468	BB289468 BB289468
, (-	15.4	85.6	337	10	BF147142	BF147142 uy07f02.y
	15.4	ω	350	10	BE556305	BE556305 sq01a05.y
,	15.4	85.6	393	10	BE650684	BE650684 UI-M-BH3-

~ 20 80	A1493734 qz12907.x AW230662 uo66080.y AQ427545 CITBI-EI- H16901 ym39b02.r1 AW395872 sh01c11.y		⊣ `	AQQ16921 C1T.HSF-2 AGQ17310 Homo sapi AGQ17312 Homo sapi BHO94331 RPCI-24-3 BGG94687 NISC_1v06 AV836265 AV836265
12 AQ442997 9 AA102952 10 BF256005 10 BF326958 9 AW738969 9 AA752987		10 C84686 12 AQ596806 10 BI784821 12 AZ446415 10 BI784791	A	12 AQ016921 12 AG017310 12 BH094331 12 BH094331 10 BG694687 9 AV836265
410 1 425 9 443 1 451 1 457 9	4000			
8885.6 85.6 85.6 85.6	888 85.0 85.0 85.0 85.0 85.0 85.0 85.0 8	885.0 855.0 855.0 855.0	855.6 855.6 855.6 85.6	855.6 855.6 855.6 85.6
15.4	112 112 12 13 14 14 15 15 15 15 15 15 15 15 15 15 15 15 15	112 123 123 14 14 15 15 15 15 15 15 15 15 15 15 15 15 15	15.4 15.4 15.4 15.4 15.4	15.4 15.4 15.4 15.4 15.4
c 18 19 20 21 23	o o	335 335 335 335 335 335 335 335 335 335	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	C 40 C 41 C 42 C 42 C 44 C 44

ALIGNMENTS

BG531376 1441 bp mRNA linear EST 03-APR-2001 602559625F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4697383 5', mRNA sequence. BG531376 BG531376 BG531376 IG:13522913 EST. human. Homo sapiens BURARYOCH, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Butheria; Primates; Catarrinii; Hominidae; Homio. 1 (bases 1 to 1441) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) National Institutes of Health, Mammalian Gene Collection (MGC) Contact: Robert Strausberg, Ph.D. Email: capabs.rdmail.nih.gov Contact: Robert Strausberg, Ph.D. Email: capabs.rdmail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: High quality sequence start: 186 High quality sequence start: 186 High quality sequence start: 186	
RESULT 1 BG531376/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES

g

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/note-vector: BlueScript SK, Site_1: Eco RI; Site_2: XhoI for The library is from early (spring) secondary wood, taken from a ten year old tree in the transitional phase. The tree is a kind gift of the Westvaco Corporation. Secondary and primary xylem was harvested from the tree by peeling back the bark and primary xylem and then removing the underlying tissue with a block plane. NoTE: The sequences contain a 'CDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTGGGCACGGG'."
                                                                                                                                                                                                                            EST 26-FEB-2001
                                                                                                                                                                                                                    BG318395 513 bp mRNA linear EST 26-FEB-2003 NXPV_013_B06_F NXPV (Nsf Xylem Planings wood Vertical) Pinus taeda cDNA clone NXPV_013_B06 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSS 16-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 513)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Coastal plain loblolly pine from North Carolina"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16.4; DB 10; Length 513;
Pred. No. 4.5e+02;
0; Mismatches 1; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Clone_INXRV_013_B06"
/Clone_Ilb="NXRV (Nsf Xylem Planings wood Vertical)"
/Clssue_IYpe="Xylem"
/Cell_Itype="Planings (secondary)"
/dev_stage="Transitional"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecular Basis of Wood Formation in the Pine Megagenome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Pinus taeda"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                558 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ajohnson@unity.ncsu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:3352"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="XL1-Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   BG318395.1 GI:13127825
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94.48;
                                                               237 ATACACTGGTCATGTTAA 254
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                                          1 atactctggtcatgttaa 18
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Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                                   loblolly pine.
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                                                                                                                                                                                                                                                                                                                                                                                                   Pinus taeda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
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                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ621441/c
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                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                       BG318395
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF516695

NXSI_002_C09_F NXSI (Nsf Xylem Side wood Inclined) Pinus taeda cDNA clone NXSI_002_C09 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NXSI_002_C09"
/clone_lib="NXSI_002_C09"
/tissue_type="Xylem"
/cell_type="Xylem"
/cell_type="Side"
/dev_stage="Juvenile"
/lab_host="Xil-Blue"
/note="Vector: BlueScript SK; Site_1: Eco RI; Site_2: XhoI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 344)
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCGGAGGGGGCGGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 k (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecular Basis of Wood Formation in the Pine Megagenome Uppublished (2000)
Contact: Johnson, Arthur North Carolina State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                         94.4%; Score 17; DB 10; Length 1441; 100.0%; Pred. No. 3e+02; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                              1 others
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                                                                                                                                                                                                      367 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: T3.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 ATACTCTGGTCATGTTA 167
                                                                                                                                                                                 Library."
381 c
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Best Local Similarity 94.48
                                                                                                                                                                                                                                                                                                                                                        17; Conservative
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Fax: 919 515 7801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    loblolly pine.
                                                                                                                                                                                                                                                                                                                                 Local Similarity
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41 a 111 c 129 g 169 t 21 others
                                                                                                                           /organism="Strongylocentrotus purpuratus"
/db_xref="taxon:7668"
/dlone="Plate=41 Col=24 Row=L"
/clone="lb="Strongylocentrotus purpuratus, purple sea
urchin, sperm qenomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 26-FEB-2001
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BG318023
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Pred. No. 4.6e+02;
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Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
                                                                 High quality sequence stop: 564.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ajohnson@unity.ncsu.edu
Plate: 41 row: L column: 24
Seq primer: SP6
Class: BAC ends
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94.48;
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Matches 17; Conservative
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Pinus taeda
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                                              Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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Cameron, R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R.,
Swartzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T., Wray,
G.A., Ettensohn, C.A., Lehrach, H., Britten, R.J., Davidson, E.H. and
Hood, L.
                                                                                                                                                                                             High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
701 Queen Anne Avenue North, Seattle, WA 98109, USA
701 (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3019 row: L column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_aref="plate=3019 Col=10 Row=L"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
           1 (bases 1 to 558)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
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Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)
                                                                                                           scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
                                                                                                                                                                                        Contact: Mahairas GG, Wallace JC, Hood L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 558.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ144687.1 GI:8296590
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Fax: (626) 793-3047
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1 (bases 1 to 404)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo saplens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 635)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. J., Zagoo, M.A., Bordin, S., Costa, F. F.,

Goldman, G. H., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, D.H.,

Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW812504 635 bp mRNA linear EST 17-MAY-2000 CM4-ST0181-231199-049-b12 ST0181 Homo sapiens cDNA, mRNA sequence. AW812504
                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="Plate=3203 Col=24 Row=E"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
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                                                                                                                                                                                                                                                                                                                            High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                       Contact: Mahairas GG, Wallace JC, Hood L
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Fax: +55-11-2707001
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                                                                                                                                                                                                                                                                                          SP_0127_A2_G12_T7A Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=127 Col=24 Row=M, DNA sequence.
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                                                                                                                                                                                                                                                                             GSS 31-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear GSS 08-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HE 3203_A2_C12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3203 Col=24 Row=E, DNA sequence.
AQ150695
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urchin, sperm genomic BAC library"
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Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Strongylocentrotus purpuratus.
Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinocea; Echinoida;
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                                                                                                                                                                                                                                                                           linear
Pred. No. 4.7e+02;
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/db_xref="taxon:7668"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strongylocentrotidae; Strongylocentrotus.
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            94.4%; Pred. ....
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Division of Biology 156-29
California Institute of Technology
                                                                                                                                                                                                                                                                           724 bp
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Location/Qualifiers
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Seg primer: T7
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Fax: (626) 793-3047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 c
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Matches 17; Conservative
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                       Best Local Similarity
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DEFINITION

AQ150695

RESULT

ACCESSION

KEYWORDS

SOURCE

VERSION

BASE COUNT

ORIGIN

FEATURES

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/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="163022"
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97044477
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Fax: 319 335 9565
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                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="$$70181"
/dev_stage="Adult"
/dev_stage="Adult"
/dev_stage="Adult"
/site_1: Smal;
/site_2: Smal;
/site_2: Smal;
/site_1: Smal;
/site_2: Smal;
/site_1: A mini-library was made by cloning products
/derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
/profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions."
/site_135 g 196 t
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This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
1. .1026
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            Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-ST0181-231
199-049-b12&t3=1999-11-23&t4=1)
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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Tetraodon nigroviridis DNA sequence
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1 (bases 1 to 1026)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
Charaterization and repeat analysis of the compact genome of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tobases 1 to 1026)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
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                                                                                                                         Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 586.
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Matches 16; Conserv
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Anote—"Vector: pTTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CTOs plinary is a non-normalized library constructed from the following rat brain tissues: embryonic day 17, embryonic day 19, embryonic day 21, adult day 1, adult be a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.ulowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear EST 19-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 bp mRNA linear EST 19-JUL-200
LI-R-CT0s-cax-d-05-0-UI.sl UI-R-CT0s Rattus norvegicus CDNA clone
UI-R-CT0s-cax-d-05-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: msoarcs@blue.weeg.ulowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the non-normalized rat brain pool library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 213)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                              86.7%; Score 15.6; DB 12; Length 1026; 93.8%; Pred. No. 1.4e+03; tive 1; Mismatches 0; Indels 0;
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/db_xref="taxon:10116"
/clone="UI-R-CTOS-cax-d-05-0-UI"
/clone_lib="UI-R-CTOS"
/dev_stage="ADULT"
/lab_host="DH10B_(Life Technologies)"
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                                                                                                                                               RESULT 13
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                                                                                                                                                                  BB024447
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                                                                                                                                                                                                                                                                                                                                                                                                         BE142340 220999-015-b05 HT0143 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM3-HT0143-220 999-015-b05&t3=1999-09-22&t4=1) Seq primer: puc 18 forwart: 102 High quality sequence start: 102 High quality sequence start: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: head_neck; Vector: puc18; Site_1: Smal; Site_2: Smal; A min!-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini, Hominidae; Homo.
1 (bases 1 to 225)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed sequence tags broc. Nail. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
                                                                                                                                                                                                            Gaps
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0
                                                                                                                                                               Length 213;
                                                                                                                                                        Score 15.*, ___
Pred. No. 1.1e+03;
. __.+ches 1; Indels
                                                                                                                                                        85.6%; Score 15.4; DB 10;
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                     TAG_TISSUE=rat brain pool TAG_SEQ=ACTTC"
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/db_xref="taxon:9606"
/clone_lib="HT0143"
/dev_stage="Adult"
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                                                                49 g
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TAG_LIB=UI-R-CT0s
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                                                                                                                                                                             94.18;
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COMMENT
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Gaps

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1; Indels

85.6%; Score 15.4; DB 9; Length 225; 94.1%; Pred. No. 1.2e+03;

0; Mismatches

Conservative

Best Local Similarity Matches 16; Conserva

Matches

Query Match

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P. Endo, T. Fukuda, S., Fukunishl, Y., Hara, A., Hayatsu, N.,
Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Kagawa, T., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Kaya, S., Kurihara, C., Kusakabe, M.
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ono, T., Owa, C., Saito, H., Sato, K., Shibata, K., Shibata,
Y., Shigemoto, Y., Shinagawa, A., Takahashi, F., Tominaga, N., Toya
T., Tsunoda, Y., Watahiki, A., Yokota, T., Yamamura, T., Yamanaka, I.,
Yano, R., Yasunishi, A., Yokota, T., Yoshino
RIKEN Mouse ESTS (Konno, H., et al.)
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genome-resegac.riken.go.jp,
URL: http://genome.gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci,P. Nishiyama.Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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                                                                                                                                                                                                                         BB02447 RIKEN full-length enriched, adult male pituitary gland Mus musculus cDNA clone 5330421N15 3', mRNA sequence.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 18-18-503-9226
Fax: 81-45-503-9216
Fmail: genome-res@gsc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 297)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="5330421N15"
/clone_lib="RIKEN full-length enriched, adult male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,
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/lab_host="DH10B"
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76 ATACTCTGGTCATCTTA 92
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Thu Aug

us-09-899-718a-8.rst

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scunneale, beunele, scutrognath; muridae; murinae; mus.

(bases 1 to 303)

Found, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci

P., Endo, T., Fetudae, S., Fetunishi, Y., Hara, A., Hayatsu, N.,

Hirozane, T., Hori, F., Ishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,

Izawa, M., Radota, K., Kagawa, T., Kai, C., Kawaka, J., Kikuchi, N.,

Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,

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Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,

Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Takahashi, F., Sugahara, Y.,

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T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I.,

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Unpublished (2000)

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Automated filtration-based high-throughput plasmid preparation
Carninci,P. and Hayashizaki,Y.

Carninci,P. and Hayashizaki,Y.
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URL:http://genome.gsc.riken.go.jp/
Carninci,b., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., MuramatSu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BB289468 RIKEN full-length enriched, 2 cells egg Mus musculus cDNA clone B020040F24 3', mRNA sequence.
BB289468 GI:8989917
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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The Institute of Physical and Chemical Research (RIKEN)
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Pred. No. 1.2e+03;
0; Mismatches 1; Indels C
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VERSION SOURCE

ORIGIN

COMMENT

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JF147142 337 bp mRNA linear EST 29-DEC-2000 uy07f02.yl McCarrey Eddy spermatocytes Mus musculus cDNA clone IMAGE:3657339 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 317)
Marra,M., Hillier, E., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood, K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter F. Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., The Washu-NrI Mouse EST Project 1999
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                  Anote—"Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5] GAGAGAGARCCAAGGACTCTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                   Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                        /clone_lib="RIKEN full-length enriched, 2 cells egg"
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Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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                                                                                                                                                  /organism="Mus musculus"
/db_xref="taxon:10090"
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Location/Qualifiers
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Fax: 314 286 1810
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FEATURES

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/issue_type="spermatocytes, pooled from multiple mice"
/dev_stage="60 day"
/lab_nost="DH10B (phage-resistant)"
/lab_nost="DH10B (phage-resistant)"
/note="organ: testis; Vector: pBluescript SK+ (Stratagene); Site_1: XhoI: Site_2: BcoRI: cDMA oligo dT-primed
[5'.(GA)10.ACTAGCTCGGTTTTTTTTTTTTTTT]; and directionally
cloned using 5' linkers 5'-AATTGGCACAGA-3' and
5'-CTGGCGG-3'. Size selection of >400bp material gives
average insert size ranging from 1-2 kb. Library was mass
average insert size ranging from 1-2 kb. Library was mass
excised (from lambda-UniARP-XR) and resulting
single-stranded phagemids were prepped and tranformed
into DH10B. Library contains 90% recombinants.
References: J. Androl. 20:635-639 and Gene 25:263-269.
Library constructed and donated by J. McCarrey, Ph.D.
(Southwest Foundation for Biomedical Research, Dept. of
Genetics); excision done by E.M. Eddy, Ph.D. (National
Institutes of Health, National Institute of Environmental
Health Sciences). Original lambda-based library is
available through ATCC, catalog #63422."
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                                                                                                                                            /clone_lib="McCarrey Eddy spermatocytes" /sex="male"
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Search completed: July 31, 2002, 12:12:16 Job time: 13489 sec

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July 31, 2002, 14:11:25; Search time 720.8 Seconds (without alignments) 42.875 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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| SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1991.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description		Human digestive ev	Minglootide ag	protection seducing	Human immine/haema	Thomas demin	וומווומוו דוומווחווב/ וומבווומ	Human 1mmune/haema	Himan immi nemil	ביייים ביייים ביייים ביייים	rusarıum venenatum	Arabidonsis thalia		Arabidopsis thatia
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ALIGNMENTS

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Human; digestive system antigen; gene therapy; cancer; appendicitis; ulcerative colitis; infection; Hirschsprung's disease; chronic colitis; digestive system disorder; Meckel's diverticulum; ds.
                                                                       Human digestive system antigen genomic sequence SEQ ID NO: 4129.
       AAK90553 standard; DNA; 32167 BP.
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2000US-0184664.
2000US-0186350.
2000US-0189874.
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2000US-0198123.
2000US-0205515.
2000US-0209467.
2000US-0214886.
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                                                                                                                                                                                                                       2000US-0179065.
                                                    (first entry)
                                                                                                                                                          WO200155314-A2.
                                                                                                                                                                                                                              04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
11-MAR-2000;
11-MAR-2000;
19-MAY-2000;
28-JUN-2000;
                                                                                                                                       Homo sapiens
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11-JUL-2000; 2000US-0217487.
11-JUL-2000; 2000US-0217496.
14-JUL-2000; 2000US-0218290.
26-JUL-2000; 2000US-0220963.
26-JUL-2000; 2000US-0220964.
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14-SEP-2000;
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18 - AUG - 2000; 2
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14-SEP-2000;
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22-AUG-2000;
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Barash SC, Ruben SM;
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08-NOY-2000; 2000US-0246611.
08-NOY-2000; 2000US-0246611.
08-NOY-2000; 2000US-0246611.
17-NOY-2000; 2000US-0249209.
17-NOY-2000; 2000US-0249209.
17-NOY-2000; 2000US-0249209.
17-NOY-2000; 2000US-0249211.
17-NOY-2000; 2000US-0249211.
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17-NOY-2000; 2000US-0249211.
17-NOY-2000; 2000US-0249214.
17-NOY-2000; 2000US-0249218.
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17-NOY-2000; 2000US-0249218.
17-NOY-2000; 2000US-0249218.
17-NOY-2000; 2000US-0249219.
17-NOY-2000; 2000US-0249264.
17-NOY-2000; 2000US-0249264.
17-NOY-2000; 2000US-0249297.
17-NOY-2000; 2000US-0249297.
17-NOY-2000; 2000US-0249299.
17-NOY-2000; 2000US-0249299.
17-NOY-2000; 2000US-0249299.
17-NOY-2000; 2000US-0249299.
17-NOY-2000; 2000US-0250391.
05-DEC-2000; 2000US-0250391.
05-DEC-2000; 2000US-0250391.
05-DEC-2000; 2000US-0250391.
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08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
05-JAN-2001; 200UUS-0259678.
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20000S-0246609
20000S-0246610
20000S-0246611
20000S-0249207
20000S-0249208
               2000US-0241809.
2000US-0241826.
2000US-0244617.
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        2000US-0241808
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2000US-0246476
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        20-OCT-2000;
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08-NOV-2000;
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WPI; 2001-502630/55

Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases - $\,$

Disclosure; SEQ ID NO 4129; 986pp; English.

The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antigen of the invention.

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RESULT
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Sequence 32167 BP; 9824 A; 5983 C; 6230 G; 10130 T; 0 other;
                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of the human heparanase gene.
                                                                                                       DB 22;
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                                                                                                Score 16.4; DE
Pred. No. 53;
0; Mismatches
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Pred. No. 55;
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94.4%;
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Best Local Similarity 94.4%;
Matches 17; Conservative
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(FRIE/) FRIEDMAN M M.
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Best Local Similarity

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                                                                                                                                            Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                            Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23323.
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Mismatches
                                                                           BP
                                Db 11410 AGACTCTGGTCATGTTAA 11393
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2000US-0218290.
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2000US-0225268.
                                                                  AAK68511/c
ID AAK68511 standard; DNA; 936
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2000US-0190076
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                1 atactctggtcatgttaa 18
                                                                                                           (first entry)
Matches 17; Conservative
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14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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22-AUG-2000;
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08-SEP-2000;
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30-JUN-2000;
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2000US-0241826.
                     08-SEP-2000; 2000US-0232081.
12-SEP-2000; 2000US-0231968.
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17-NOV-2000; 2000US-0249245
            08-SEP-2000; 2000US-0231414
                                           2000US-0232400
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amino acid sequences given in AmM82170 to AMM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention. (I) proteins and polynucleotides may be used in the prevention. (I) proteins and polynucleotides may be used in the prevention. (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally. (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to produce the secreted (I), by cepress the diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK84950 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAK54951 to AAK64702 encode the human immune/haematopoletic antigen (I)
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                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen CA, Barash SC, Ruben SM;
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2000US-0251989.
2000US-0251990.
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                                                                                                                 2000US-0250391.
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2000US-0251479.
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                                     2000US-0249297
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05-DEC-2000;
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08-DEC-2000;
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05-DEC-2000;
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17-NOV-2000;
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AAK57354/C
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cytostatic; gene therapy; vaccine; metastasis; ss.

May MOZOUS T182-A2.

PM WOZOUS T182-A2.

PM UZAN-2001, 200100-011354.

PM 14-M2-2002, 2000018-011565.

PM 15-MAR-2003, 2000018-011565.

PM 15-MAR-2003, 2000018-011561.

PM 15-MAR-2003, 2000018-011581.

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PM 15-MAR-2003, 2000018-011581.

PM 15-MAR-2003, 2000018-011583.

PM 15-MAR-2003, 2000018-011583.

PM 15-MAR-2003, 2000018-011583.

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PM 15-MAR-2003, 2000018-021861.

PM 15-MAR-2003, 2000018-021861.

PM 15-MAR-2003, 2000018-021829.

PM 16-MAR-2003, 2000018-02189.

PM 16-MAR-2003, 2000018-02189

2000US-0235484 2000US-0235836 2000US-0235836 2000US-0236369 2000US-0236369 2000US-0236369 2000US-0236369 2000US-0236369 2000US-0237039 2000US-0237039 2000US-0237039 2000US-0237039 2000US-0237039 2000US-0237039 2000US-0237039 2000US-0237039	200005-0241230 200008-0241785 200008-0241786 200008-0241809 200008-0241809 200008-0246474 200008-0246474 200008-0246474 200008-0246474 200008-0246476 200008-0246476 200008-0246526	Reserved
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ANK ANK54951 to ANK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
cartivity, and can be used in gene therapy and vaccine production. (I)
cartivity and can be used in gene therapy and vaccine production. (I)
cartive and polynuclectides may be used in the prevention, diagnosis and
carample, they may be used to treat disorders associated with decreased
carample, they may be used to treat disorders associated with decreased
carpession by rectifying mutations or deletions in a patient's genome
cut a ffect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
polynuclectides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynuclectides may be used to prevent,
cancers and cancer metastases of haematopoietic-derived cells. AAK64703
cancers and cancer metastases of haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK84950 and AAM82169
crepresent sequences used in the exemplification of the present invention.
                                                                            Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                 Claim 1; SEQ ID NO 2414; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                            Sequence 407 BP; 105 A; 102 C; 56 G; 140 T; 4 other;
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                          Rosen CA, Barash SC, Ruben SM;
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(HUMA-) HUMAN GENOME SCI INC.
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Matches 16; Conservative
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                                                            P-PSDB; AAM84573
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haemacopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 cancers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK5492 to AAK54950 and AAM81269 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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88.9%; Pred. No. 2.5e+02;
ive 0; Mismatches 2; Indels 0)
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Best Local Similarity 88.9
Matches 16; Conservative
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
coplamical caids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic related diseases, especially
cancers and cancer metastases of haematopoietic antigen genomic
sequences from the present inmunne/haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK64703
conserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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2000US-0249211.
2000US-0249212.
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82.2%; Score 14.8; DB 22; Length 474; 88.9%; Pred. No. 2.5e+02; iive 0; Mismatches 2; Indels 0;

Query Match 82.2 Best Local Similarity 88.9 Matches 16; Conservative

represent sequences used in the exemplification of the present invention.

Sequence 474 BP; 135 A; 109 C; 90 G; 140 T; 0 other;

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The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTS are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the Same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production of the global expression of genes from FF cells allows the production corrected, possible functions of unknown open reading frames can be described and gene copy number variation and stability can be identified and gene copy number variation and stability can be dantified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore compineering. Using ESTS provides several advantages over genomic or array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate conditions, analysis of the results. AAF01247 represents ESTS from the conditions of the gene products from Aspergillus of the samilarat to harriagal represents ESTS from the conditions of the ferme from the form fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags \cdot
                                                                                                                                                                                                                                                                                                                                                                                               Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
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                  Indels
                                                                                                                                           Arabidopsis thaliana DNA fragment SEQ ID NO: 4839.
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27-MAY-1999;

28-MAY-1999;

28-MAY-1999;

27-MAY-1999;

28-MAY-1999;
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                             AAC34572;
       AAC34572
RESULT
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us-09-899-718a-8.rng

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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
          Arabidopsis thaliana DNA fragment SEQ ID NO: 983.
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9905-0139459.
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990S-013722.
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99US-0132048.
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                                                                                                     25-FEB-2000; 2000EP-0301439.
17-OCT-2000 (first entry)
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07-JUN-1999;
08-JUN-1999;
10-JUN-1999;
10-JUN-1999;
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                                                                                                                      25-FEB-1999;
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14-MAY-1999;
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18-MAY-1999;
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                                                                           EP1033405-A2.
                                                                                          06-SEP-2000
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0
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88.9%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; br
2.7e+02;
2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC32880 standard; DNA; 1382 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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9908-0161404.
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9908-0161359.
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99US-0161992
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9903-0154039.
9903-015479.
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9903-0155659.
9903-0155659.
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                                                                      99US-0151080
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          99US-0149723
                                                                                                                                                                                                                                           99US-019
99US-01
                                                                                                                                                                                                                                                         99US-01
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21-OCT-1999;
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08-0CT-1999;
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25-AUG-1999;
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27-AUG-1999;
                                                                              30-AUG-1999;
31-AUG-1999;
                                                                                                                                                                                -SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Si
Matches 16;
                                                                                                             10-SEP-1999;
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XX
AC AAC3:
              δλ
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990S-0139763. 99US-0139817. 99US-0139817. 99US-0140353. 99US-0140353. 99US-0140363. 99US-014023. 99US-014023. 99US-01421287. 99US-01421287. 99US-0142139. 99US-0142139. 99US-0142139. 99US-014231. 99US-014331. 99US-0144085. 99US-0144085. 99US-0144085. 99US-0144085. 99US-0144085. 99US-0144086. 99US-0144086. 99US-0144086. 99US-0144086. 99US-0144086. 99US-0144086. 99US-0144086. 99US-0145086. 99US-0147088.	990S-014/79 990S-01483 990S-01483 990S-014863 990S-01493 990S-01493 990S-01494 990S-01497 990S-014997 990S-014997 990S-014997
R 22-JUN-1999, R 22-JUN-1999, R 22-JUN-1999, R 23-JUN-1999, R 23-JUN-1999, R 23-JUN-1999, R 28-JUN-1999, R 29-JUN-1999, R 20-JUN-1999, R 20-JUN-1999,	UG-1999; UG-1999; UG-1999; UG-1999; UG-1999; UG-1999; UG-1999; UG-1999; UG-1999; UG-1999; UG-1999; UG-1999; UG-1999;
	PR PR PR PR PR PR PR PR

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Gaps
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88.9%; Pred. No. 2.7e+02;
ive 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana DNA fragment SEQ ID NO: 45288.
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990S-0161992.
990S-0161993.
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Best Local Similarity 88.99
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19-Jul. 1999;

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29-Aug. 1999;

11-Aug. 1999;

20-Aug. 1999;
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22 - JUN - 1999;

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28-MAY-1999;

29-MAY-1999;

20-JUN-1999;

21-JUN-1999;

21-JUN-1999;
                                             EP1033405-A2
                                                              06-SEP-2000
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and insecticides, therapeutics and pharmaceutical drugs. The invention is sequences genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                     (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Consensus; resistance; fungus; pathogen; wheat; cell wall; apposition; papilla; contact site; callose; carbohydrate; phenol; transgenic plant; Mlo; Erysiphe graminis; powdery mildew; ss.
                                                                                                                                                                                                                                                                                                                                         82.2%; Score 14.8; DB 23; Length 1926;
88.9%; Pred. No. 2.8e+02;
Live 0; Mismatches 2; Indels 0;
                                                                                                                                                          Claim 1; SEQ ID NO 29374; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana Mlo fungal resistance gene CIB10295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= "Mlo fungal resistance protein"
                                                                                                                                                                                                                                                                                                        Sequence 1926 BP; 394 A; 531 C; 565 G; 436 T; 0 other;
                                                                                Li PWD, Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmeron JM, Weislo LJ, Strawn LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                         23-MAR-2000; 2000US-191637P. 11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                           1 atactctggtcatgttaa 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 88.9
Matches 16; Conservative
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                                                                             Venter JC, Adams M,
                                                                                                 WPI; 2001-656860/75.
                                                          (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 14.8; DB 21; Length 1554;
Pred. No. 2.8e+02;
0; Mismatches 2; Indels 0;
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99US-0159584.
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99US-0160770.
  99US-0153758
                                                                                            99US-0157117.
                                                     99US-0155486.
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99US-0160981.
99US-0160989.
                                                               99US-0155659
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99US-0161406
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hes 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pharmaceutical; gene; ds.
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                                                           24-SEP-1999;
28-SEP-1999;
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04-OCT-1999;
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13-OCT-1999;
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Kramer CM;

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WO200157182-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wheat; fungal resistance; fungal pathogen; Erysiphe graminis; papillae; powdery mildew; Mo; cell wall apposition; transgenic plant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polynucleotide which encodes Mlo protein from wheat, useful for producing fungal resistant plants, in particular wheat plant
                                                                              This sequence represents the coding region for the Arabidopsis thaliana fungal resistance gene CIB10295. The Mio protein confers resistance to fungal resistance by stimulating the formation of large cell wall appositions, designated papillae, at the conteact site with the fungal pathogen. These papillae, at the contain pathogen and these papillae mainly contain callose, but also contain pathogen. These papillae mainly contain callose, but also contain carbohydrate, phenols and proteins and are used to prevent penetration of the fungal hyphae into the plant. The new Mio sequences are used to generate transgenic plants resistant to fungal pathogens, especially
                                                                                                                                                                                                                                                                     Gaps
                        New proteins useful for generating transgenic plants resistant to
                                                                                                                                                                                                                                         82.2%; Score 14.8; DB 20; Length 1935;
88.9%; Pred. No. 2.8e+02;
Live 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequence of the Arabidopsis Mlo protein CIB10295.
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                                                                                                                                                                                                         Sequence 1935 BP; 576 A; 382 C; 398 G; 579 T; 0 other;
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Patton DA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "Mlo protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weislo LJ, Strawn LJ,
Levin JZ, Heifetz PB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
89..1810
                                                                  Claim 3; Page 78-81; 102pp; English.
                                                                                                                                                                                          Erysiphe graminis (powdery mildew).
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Matches 16; Conservative
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WPI; 1999-571820/48.
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                                                 fungal infection
               P-PSDB; AAY26970.
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Vernooij BT,
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The present sequence encodes a Mlo protein. Mlo proteins given resistance to fungal pathogens which infect living epidermal plant cells. Mlo proteins give proteins resistance to fungal pathogens, especially Mlo proteins give proteins resistance to fungal pathogens, especially locus are responsible for a plant resistant pathotype. The mechanism of Muo resistance linvolves the formation of large cell wall appositions, of Mlo resistance linvolves the formation of large cell wall appositions, called papillae, at pathogen contact sites. Papillae mainly contain callos, but also carbohydrates, phenols and proteins. Polynucleotides encoding Mlo proteins are useful for making transgenic plants, preferably wheat, which are resistant to fungal pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                                                                                                                                                                                                                                                                                                 Query Match 82.2%; Score 14.8; DB 22; Length 1935; Best Local Similarity 88.9%; Pred. No. 2.8e+02; Metches 16; Conservative 0; Mismatches 2; Indels 0;
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14-AUG-2000; 2000US-0225757.
14-AUG-2000; 2000US-0225758.
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2000US-0180628.
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2000US-0231242.
2000US-0231243.
2000US-0231244.
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2000US-0231414.
2000US-0232080.
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2000US-0232399.
2000US-0232400.
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08 NOV 2000; 2000US-0246474.

08 NOV 2000; 2000US-0246476.

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08 NOV 2000; 2000US-0246477.

08 NOV 2000; 2000US-0246478.

08 NOV 2000; 2000US-0246524.

08 NOV 2000; 2000US-0246526.

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2000US-0244617
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01-SEP-2000;
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08-NOV-2000; 2
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AMES AMES 10 AAMES 170 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAMES 170 to AAMES 10: (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased that affect the activity of (I) by expressing in a patient's genome complement the patients own production of (I). Additionally, (I) explained the proteins or to polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the composer and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAMES 4703 concers from the present invention. AAMES 481 to AAMES 169 crepresent invention. AAMES 482 to AAMES 482 crepresent invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis
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2000US-0249209.
2000US-0249210.
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2000US-0249265.
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2000US-0250160.
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: 2000us-0251989.
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2000US-0251868.
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08-NOV-2000;
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17-NOV-2000;
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AL512443 Human DNA
AL605722 Danio rer
AC025010 Home sapi
AC094963 Rattus no

AC025010 AC094963 AL359456_1 AC091696

AL591420 AL512443 AL606722

Sequence Zebrafish

AC091696 Felis cat AL591028 Homo sapi AC097356 Homo sapi AC020698 Homo sapi

Ac036175 Homo sapi

AC020698 AC036175

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Human DNA AC108072 Homo sapi

AL356053 AC106149 AP002508

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Homo sapi Mus muscu

AC019106 AC099697

Homo sapi

AC090229 AC090370 AC019106 AC099697

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Human DNA Human DNA

AL596243 AL589848 AC091955 AL662913 F

AL596243 AL589848 AC091955 AL662913 AC011929 AC073403 AC016725 AL662896

Homo sapi Homo sapi Homo sapi Homo sapi

AC011229 Homo sapi AC073403 Homo sapi AC016725 Homo sapi AL662896 Homo sapi AC094034 Rattus no AC007684 Homo sapi

AF176522 Mus muscu

AC007684 AF176522

CCZP2A

10 5

AC094034

Z72491 C.carpio mR Z72493 C.carpio mR AB041571 Mus muscu AJ250379 Bos tauru Z72494 C.carpio ZP Human cos Oryza sat Homo sapi Homo sapi

HSAC000358

CCZPZGEN

AY013245 AC090724 AC102336

43284 50000 53949 65020 67895

AP004160

AB041571 BTA250379

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July 31, 2002, 14:02:11; Search time 6034.22 Seconds (without alignments) 62.424 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                 1797656 seqs, 10463268293 residues
                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                               OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                         IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                              1 atactctggtcatgttaa 18
                                                                                                                                     US-09-899-718A-8
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Maximum DB seq length: 2000000000
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em_htg_other:*
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Score Match Length DB
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gb_sts:*
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                                                                                                                                 Title:
Perfect score:
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                                                                                                                                                             Sequence:
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                                                                             Run on:
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PAT 06-FEB-2002 artificial sequence.

1 (sites)
Sprunck, S., Kluth, A., Becker, D., Luetticke, S. and Loerz, H.
Promoters of gene expression in plant caryopses
Patent: WO 0202785-A 8 10-JAN-2002;
Aventis CropScience GmbH (DE)
Location/Qualifiers linear DNA 7 t Sequence 8 from Patent W00202785. AX349070 AX349070.1 GI:18615105 ы Б synthetic construct. 3 C α AX349070 DEFINITION source ACCESSION VERSION ORGANISM RESULT AX349070 LOCUS BASE COUNT KEYWORDS SOURCE JOURNAL REFERENCE AUTHORS FEATURES TITLE ORIGIN

Result

DEFINITION

KEYWORDS VERSION

AX349063

RESULT

δλ

REFERENCE AUTHORS JOURNAL

FEATURES

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repeat_region
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cambridgeshire. CBIO 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

nov 17, 2001 this sequence version replaced gi:15721150.

Where differences arsembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

wariation annotation may not be found in the sequence submission

variation annotation may not be found in the sequence submission

variation annotation may not be found in the sequence submission

variation annotation may not be found in the sequence submission

variation annotation may not be found in the sequence with corresponding to the overlapping clone, as we submit sequences with

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.
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Sebrafish DNA sequence from clone XX-221H6 on chromosome 7 Contains a novel gene similar to nitr3r.1 (novel immune-type receptor 3r.1), a novel gene similar to nitr3r.1 (novel immune-type receptor 3r.1), a novel gene similar to nitr3 and part of two novel genes similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopergyli; Neopterygli; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
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                                                                                                                                                                                                                                                            PAT 06-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                         Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sprunck, S., Kluth, A., Becker, D., Luetticke, S. and Loerz, H.
                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 18; DB 6; Length 3785; 100.0%; Pred. No. 8.2; tive 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                       linear
100.0%; Score 18; DB 6; Length 18; 100.0%; Pred. No. 6;
                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           promoters of gene expression in plant caryopses
Patent: WO 0202785-A 1 10-JAN-2002;
Aventis Cropscience GmbH (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG; immune-type receptor; nitr3; nitr3r.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     961 t
                                                 0; Mismatches
                                                                                                                                                                                                                                                                                 Sequence 1 from Patent W00202785.
AX349063
                                                                                                                                                                                                                                                                               3785 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:4565"
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AL591420.5 GI:16973933
                                                                                                                                                                                                                                                                                                                                                     AX349063.1 GI:18615098
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Matches 18; Conserv
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                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
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COMMENT

7

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regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following absembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given subcreated with their source databases: Em: EMBL: Sw:, in the feature table with their source databases: Em: EMBL: Sw: database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep XX-221H6 is from a zebrafish PAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="mgLQDCFTFFLLFRYGTCEEDFIHQQPLVVAELGSSVTLPCFH SDDFTTTISWYKHGAGKRFLLIABAPNSGSVTVQYAFNNTNRFFTTTASGSYNLSTL SDDFTTTTISWYKHGAGKRFLLIABAPNSGSVTYQYAFNNTNRFFTTASGSYNLSTL STLLXEDFANYYCAKFFLNIMMFGEGTTLLHWETDRNISTSYSAPSFWTPVVCILLIS VISTYMNIVLVIQKSRKKETTEQLRSQINQIKTDDLNYAALHFSKTKPTTSRRSSMKT IQETIYSETTVH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence=not_experimental
/product="SC:dZ221H6.1 (novel immune-type receptor similar
to nitr3r.1)"
                                                                                                                                                                                                                                                                                                                                   VECTOR: pCYPAC-6

WECTOR: pCYPAC-6

WHOORPART: This sequence is not the entire insert of clone XX-221H6

It may be shorter because we sequence overlapping sections only

It may be shorter because we sequence overlapping sections only

once, except for a short overlap.

The true right end of clone XX-221H6 is at 51019 in this sequence.

The true right end of clone XX-139E19 is at 2000 in this sequence.

This clone was isolated from the BUSM1 library (C. Amemiya) and

provided by C. Amemiya (Amemiya lab, Virginia Mason Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inconsistency in the number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .2825,3152. .3505,4439. .4573,5294. .5328,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 copies 4 mer tata 91% conserved"
0. 2825,3152. 3505,4439. 4573,5294. 5328,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Inconsistency in the number of bases in mononucleotide run between subclones."
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/note="29 copies 2 mer at 81% conserved" 7894. .7919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3041. .3144
/note="52 copies 2 mer tt 62% conserved"
4000. .4019
/gene="SC:dZ221H6.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="16 copies 4 mer atat 75% conserved"
588. .631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             match: proteins: Tr:CAD12598 Tr:AAK60113"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="50 copies 2 mer ta 91% conserved"
1163. .1260
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/note="3 copies 14 mer 100% conserved"
complement(4020. .4061)
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1256
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1256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="match: cDNAs: Em:AF318401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="CAD21620.1"
/db_xref="G1:18369621"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="SC:dZ221H6.1"
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/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SC:dZ221H6.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1. 51019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="XX-221H6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="9
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On Oct 29, 2001 this sequence version replaced gi:14529902.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality >- as compressions and repeats; all regions were covered by at least assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; TI:, TREMBL; WP:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL512443 55613 bp DNA linear PRI 26-OCT-2001
Human DNA sequence from clone RP11-108P2 on chromosome 1, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (26-007-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                           /note="TDR1 repeat: matches 727. .934 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Day repeat: matches 147. .406 of consensus" 27825. .27883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="DANA repeat: matches 1. .59 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5; Length 51019;
                        /note="29 copies 2 mer ga 69% conserved" 19721. .19776 /note="4 copies 14 mer 80% conserved" 21020. .2127
                                                                                                                                                       21332, 21377

/note="23 copies 2 mer aa 80% conserved"

21756, 21803

/note="4 copies 12 mer 91% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="23 copies 2 mer ta 80% conserved"
23406. .23531
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                                                                                                                                                                                                                                                                                                                                         /note="17 copies 2 mer ca 97% conserved"
22702. .22867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="6 copies 21 mer 70% conserved" 23996. 24067 /note="6 copies 12 mer 100% conserved" 25897. 25968
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22354. .22387
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22912. .22957
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AL512443.7 GI:16508240
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Matches 17; Conservative
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join(17884. 17929,18244. 18597,20317. .20670,20748. .20846,
21488. .21523,21967. .22089)
/gene="Sc:dz221H6.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(17884. 17929,18244. .18597,20317. .20670,20748. .20846,
21489. .21523,21967. .22089)
/gene="SC:dZ221H6.4"
                                                                                                                                                                                                                                                                                                                                                       /db_xxef="c1:18869622"
/translation="cTCEEDFIHQOPLVLAELGSSVTLPCFHSDDFVTTISWYKHSAG
KRPLLIAYSDFNSGRVTYRNAFNNTNRFFITVASGSYNLTIHLEKEDFATYYCVKDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence-not_experimental
/product="Sc:d2221H6.3 (novel immune-type receptor)"
/product="Sc:d2221H6.3 (novel immune-type receptor)"
/db_xref="G1:18369623"
/db_xref="G1:18369623"
/franslation="ETDRISSTSVIQOPVSDRLHPGDSVTLQCSVSSHICAGHYRVYW
FKHSGYSOPGIIYTHDNRSDQCLESSERSSFVQSCVYSLSGTEJTTSDAGVYYCAVD
FCGKIRRGNGTRLTIEBSSLAMSPVLILEVISAVSIIVNIFLIIRTYCKE"
COMPLEMENT (13097. .13274)
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/db.xref="G1:18369624"
/translation="MSLOSSFFFFLIFAYGTCEEDFIHQOPLVVAELGSRVTLPCFH
SDDYVTTVSWTKHSAGKRFLLLAYSDFNSGRVTYQNAFNTNNFFITVASGSYNLTI
HLEKEDFATYYCVKDFLNRLAFGEGTILLRRETDRISSTSVLQQPVSDRLHSGSSYT
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LVLQNRRKETTEQLRGQINQIETDDLNYAALHFSKTKPSTSRRSSIKTIQETIYSETT
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/product="SC:d2221H6.4 (novel immuntype receptor similar
to nitr3)"
                                                                                                                                                 /gene="SC:d2221H6.2"
/note="predicted by Pfam
match: proteins: Tr:CAD12524 Tr:CAD12506 Tr:CAD12582
                                                                                                                                                                                                                                                                                  /evidence=not_experimental
/product="SC:dZ221H6.2 (novel immune-type receptor)"
/protein_id="CAD21621.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="predicted by Pfam
match: proteins: Tr:AAK60111 Tr:AAK60112 Tr:CAD12599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="DANA repeat: matches 322. 405 of consensus"
join(10373. 10727,10812. 10913)
/gene="SC:64221H6.3"
join(<10373. 10727,10812. >10913)
/gene="SC:64221H6.3"
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/note="DANA repeat: matches 89. .406 of consensus"
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19173. 19252
//note="DANA repeat: matches 322. .405 of consensus"
19325. .19382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"DANA repeat: matches 10. .377 of consensus"
16279. .16574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16568. 16622 / Anotes DANA repeat: matches 5. .59 of consensus"
'note="13 copies 2 mer tt 100% conserved"
                   3572. 8637
/note="33 copies 2 mer tt 68% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="match: STS: Em:G40916"
14549. .14869
                                                                                                  /gene="SC:dZ221H6.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                               LNRLMFGEGTILLCK"
                                                                                                                                                                                                                                                            /codon_start=3
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Homo sapiens chromosome 4, clone RP11-85D17
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                                                                                                                                                                                                                                                          /note="assembly_fragment:01316
fragment_chain:1"
3250. 14161.
/note="assembly_fragment:00988
fragment_chain:1"
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fragment_chain:1"
32798. .52684
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fragment_chain:1"
52785. .66125
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/note="assembly_fragment:01886
fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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                                                                                                                       /organism="Danio rerio"
/db_xref="taxon:7955"
                                                                                                                                                                                                                   /clone_lib="Amemiya"
                                                                             Location/Qualifiers
                                                                                                                                                                                             /clone="XX-27N24"
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                                                                                                                                                                          /chromosome="1
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Best Local Similarity 94.4%
Matches 17; Conservative
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                                                                                                          73309
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                                                                                                                                                                                                  IMPORTANT: This sequence is not the entire insert of clone RPI-108P2 It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true left end of clone RPII-38609 is at 53614 in this sequence. The true right end of clone RPI-333A15 is at 2000 in this sequence. Location, Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygli; Neopterygli; Teleostei; Buteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Assembly program: Natural Statistics
Assembly program: Natural May 108 of reads
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 72055 bases at least 040
Consensus quality: 72273 bases at least 030
Consensus quality: 72297 bases at least 020
Insert size: 72609; sum-of-contigs out of linear size: 88868; 5.% error; agarose-fp
Loality coverage: 11.34x in 020 bases; sum-of-contigs Quality
Coverage: 9.50x in 020 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (19-DEC-2001) Wellcome Trust Sanger Institute, Hinxton,
Submitted (19-DEC-2001) Mellcome Trust Sanger is:
Cambridgeshire, CB10 158, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Dec 21, 2001 this sequence Version replaced 9::15626247.
                                                                                              http://www.sanger.ac.uk/HGP/Chrl
http://www.sanger.ac.uk/HGP/Chrl
RPII-108P2 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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                                                                                                                                                                     http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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10125 c 9972 g 17323 t
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                            /chromosome="1
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SOURCE

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AC025010 81017 bp DNA linear HTG 13-JUL-2000
HOMO Sapiens chromosome 4 clone RP11-85D17 map 4, LOW-PASS SEQUENCE
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2 (bases 1 to 81017)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Barren, B., Linton, L., Barna, N., Bastien, V., Beda, F.,

Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,

Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G.,

Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,

Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,

Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,

Galagan, J., Gardyna, S., Glnde, S., Coyette, M., Graham, L.,

Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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* NOTE: This is a 'working draft' sequence.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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COMMENT

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Levine, R., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., McCarthy, M., McEwan, P., McGurk, A., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, N., Meldrim, J., Meneus, L., Mihova, T., Mirada, C., Mlenga, V., Morrow, J., O'Nonin, T., Noylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N., Stojanovic, N., Sherer, B., Spencer, B., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Talamas, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Direct Submission, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                            Submitted (03.4A.).
Submitted (03.4A.).
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                             Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This record contains 94 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low pass sequence sampling is useful for identifying clones that may be gene-rich and allows However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap of 100 bp 11567: contig of 758 bp in length 7: gap of 100 bp 74.3°. contig of 766 bp in length
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2534 3310: contig of 777 bp in length
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contig of 763 bp in length
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of 755 bp in length
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11142: gap of 100 bp
11910: contig of 768 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www-seq.wi.mit.edu
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Center project name: L7756
Center clone name: 85_D_17
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5899: con
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17901 18000: gap of 100 bp 18001 1876: contig of 767 bp in length 1878 18867: gap of 100 bp 1868 19642: contig of 775 bp in length 19743 19742: gap of 100 bp 19743 20493: contig of 751 bp in length 20694 20593: gap of 100 bp 20594 20593: gap of 100 bp 20594 21337: contig of 744 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27376 27475: gap of 100 bp 28238: 2016 28238: 2016 28238: 2016 28239 28338: 2016 28239 28338: 2016 29105 29105 29204: gap of 100 bp 29105 29206: gap of 100 bp 29205 29206: gap of 100 bp 29200 30699: gap of 100 bp 30838: 3037: contig of 766 bp in length 30938: 3170: contig of 785 bp in length 30938: 3170: contig of 789 bp in length 31810: gap of 100 bp 32577; 32666: contig of 785 bp in length 32577; 32666: contig of 785 bp in length 32577; 32666: contig of 785 bp in length 33567; 33461: contig of 785 bp in length 33567; 34337: gap of 100 bp 34337: contig of 776 bp in length 34338: 34438: 35216: contig of 776 bp in length 3438: 35216: contig of 776 bp in length 35217; 35316: can of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                        Jap of 100 bp 100 contig of 758 bp in length 200 contig of 768 bp in length 300 contig of 768 bp in length 300 contig of 748 bp in length
5349 15448: gap of 100 bp
5449 16206: contig of 758 bp in length
6207 16306: gap of 100 bp
                                                                 contig of 748 bp in length
                                                                                                   contig of 746 bp in length
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22202: contig of 765 bp in length
02: gap of 100 bp
23072: contig of 770 bp in length
                                                                                                                                                                                                                                                                                                                                                72: gap of 100 bp
23941: contig of 769 bp in length
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3ap of 100 bp
1: contig of 761 bp in length
100 bp
1: contig of 756 bp in length
7: contig of 756 bp in length
3ap of 100 bp
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66516 27375: contig of 760 bp in length
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contig of 749 bp in length
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   15349 15448: gap of 15449 16206: conf
                                                                             17154: gap of
17900: cont
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27476 28238: cont
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39563: 7
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37815: cont
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46487: ~--
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43030: cont
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44770: cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 81017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to of 100 bp contig of 754 bp in length ap of 172 bp in length contig of 772 bp in length
                                                                                                                                                                                                                                                                                                                                                                              55154: gap of 100 bp
55921: contig of 767 bp in length
56021: gap of 100 bp
56781: contig of 760 bp in length
56881: gap of 100 bp
57638: contig of 757 bp in length
                                                                                                                                                                                                                                                                                                                                     54: 9ap of 100 bp in length 54: 9ap of 100 bp
                                                                                                                                                                                                                   51719: gap of 100 bp 52473: contig of 754 bp in length 52573: qap of
                                                                                                                                                                                                                                                                                         p of 100 bp contig of 771 bp in length
                                                                                                                                                                                                                                                                52474 52573: gap of 100 bp
52574 53327: contig of 754 bp in length
                                                                                                     p of 100 bp contig of 755 bp in length p of 100 bp
                                                                                                                                              49983: gap of 100 pp
50748: contig of 765 bp in length
                                                                                                                                                                           50848: gap of 100 bp 51619: contig of 771 bp in length
47340: contig of 753 bp in length
                             47341 47440: gap of 100 bp
47441 48171: contig of 731 bp in length
48172 48271: gap of 100 bp
48772 49028: contig of 757 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 92;
0; Mismatches
                          100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 16.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59365 59464: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58592: gap of 59364: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC094963.3 GI:17941764
                                                                                                     128: gap of 49883: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57639 57738: gap of 57739 58492: con
                                                                                                                                                                                                                                                                                                    53427: gap of
54198: cont
                                             47441 481/1. - - 48172 48271: gap of 48172 49028: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DD 12578 AGACTCTGGTCATGTTAA 12595
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                                                                                                           49029 49128:
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Best Local Similarity
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RESULT

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* NoTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NoTE: This is a 'working draft' sequence. It currently

* NoTE: This is a 'working draft' sequence. It currently

* consists of 56 contigs. The true order of the pieces

* consists of 56 contigs. The true sequence record is

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Consensus quality: 82923 bases at least Q40 consensus quality: 92369 bases at least Q30 consensus quality: 99065 bases at least Q20 Estimated insert size: 70929; sum-of-contigs estimation Quality coverage: Ox in Q20 bases; agarose-fp estimation Quality coverage: O.8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Worley, K.C. Direct Submission Department Submitted (15-SEP-2001) Human Genome Sequencing Center, Department Submitted (15-SEP-2001) Human Genetics, Baylor College of Medicine, One of Molecular and Human Genetics, Baylor College of Medicine, One Havlor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baylor Plaza, Houston, TX 77030, USA on Dec 20, 2001 this sequence version replaced gi:17062175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assembly program: Phrap; version 0.990329First call to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8785: gap of unknown length 12107: contig of 3322 bp in length 12207; gap of unknown length 15728: contig of 3521 bp in length 15828; gap of unknown length 20121: contig of 4293 bp in length 22221; gap of unknown length 222826: contig of 2605 bp in length
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of 2145 bp in length
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contig of 3486 bp in 1
gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Baylor College of Medicine
Center code: BCM
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gap of unknown length
contig of 1533 bp in length
gap of unknown length
contig of 1129 bp in length
gap of unknown length
gap of unknown length
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5: gap of unknown length
7: contig of 1547 bp in length
8: contig of 1547 bp in length
9: gap of unknown length
9: contin of 1547 bp in length
9: contin of 1547 bp in length
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contig of 1258 bp in length
gap of unknown length
contig of 1121 bp in length
gap of unknown length
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bp in length
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bp in length
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gap of unknown length
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of 1640 bp in length
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contig of 2333 b
contig of unknown l
contig of unknown l
contig of 1668 b
gap of unknown l
contig of 1056 b
gap of unknown l
contig of 1056 b
gap of unknown l
contig of 1873 b
gap of unknown l
contig of 1873 b
gap of unknown l
contig of 1878 b
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contig of 1876 b
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contig of 1728 b
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gap of unknown
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gap of, unknown
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91699:
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from base 100001 (AL359456 Homo sapiens chromosome
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Felis catus clone RP86-117J4, WORKING DRAFT SEQUENCE, 8 unordered
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Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W.,
Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S.,
Guan, X., Gupta, J., Ho, S.-L., Idol, J.R., Karlins, E., Lee-Lin, S.-Q.,
Legaspi, R., Lim, M., Maduro, Q.L., Maduro, V.B., Masiello, C.,
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Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis
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                            92828: contig of 1029 bp in length 92928; gap of unknown length 94150: contig of 1222 bp in length 94250; gap of unknown length 94250; gap of unknown length 95381: contig of 1131 bp in length 95491: gap of unknown length 95691: gap of unknown length 97819: contig of 1228 bp in length 97819: gap of unknown length 97819: gap of unknown length 99513: contig of 1594 bp in length 100697: contig of 1684 bp in length 100797: gap of unknown length 102335: gap of unknown length 102335: gap of unknown length 102335: gap of unknown length 103359: gap of unknown length 10344: contig of 1074 bp in length 104544: contig of 1035 bp in length 10694: contig of 1035 bp in length 10694: contig of 1035 bp in length 10644: gap of unknown length
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Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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AC091696
AC091696.1 GI:14150418
HTG: HTGS_PHASEI; HTGS_DRAFI.
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94.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Continuation (2 of 6) of AL359456
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Best Local Similarity 94.4;
Matches 17; Conservative
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Matches 17; Conservative
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AL359456_0
AL359456_1
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AL359456_4
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AL359456_1
WPCOMMENT
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HTG 19-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138/16 bp DNA linear HTG 19-DEC-2 Homo sapiens chromosome 10 clone RP13-143F22, *** SEQUENCING IN PROGRESS ***, 11 unordered pieces.
ALS9102R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 13454 bases at least 040
Consensus quality: 137107 bases at least 020
Consensus quality: 137107 bases at least 020
Insert size: 137716; sum-of-contigs
Insert size: 151380; Jr. 0% error; agarose-fp
Quality coverage: 5.19x in Q20 bases; sum-of-contigs Quality
coverage: 4.77x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                            91.1%; Score 16.4; DB 2; Length 137140; 94.4%; Pred. No. 95;
                                                                                                                                                                                                                                                                                              ;
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35363 35462: gap of 100 bp
35463 43765: contig of 8303 bp in length
                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                           709 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Wellcome Trust Sanger Institute
                                                                  Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
------ Project Information
                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Summary Statistics
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/note="assembly_fragment"
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vector_side:right"
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                                                                                                                                                                                                                                                                                                                                                                                                   Db 65046 ATACTCTGGTCATGTTGA 65029
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Best Local Similarity 94.44
Matches 17; Conservative
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
                   Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Prasad,A., Shevchenko,Y., Snyder,B., Stantripop,S., Thomas,J.W., Thomas,P.J., Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                    Direct Submission
Submitted (19-MAY-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert size: 133000, agarose-fp agarose-fp agarose-fp (bality coverage: 11.63x in Q20 bases; agarose-fp quality coverage: 11.33x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequencing vector: plasmid; n/a; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 consensus quality; 133760 bases at least 040 consensus quality; 134423 bases at least 030 consensus quality; 13418 bases at least 020
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3: gap of unknown length
5: contig of 6587 bp in length
6: gap of unknown length
5: contig of 10935 bp in length
5: contig of 10642 bp in length
7: gap of unknown length
7: gap of unknown length
7: gap of unknown length
8: contig of 16642 bp in length
8: contig of 16642 bp in length
9: contig of 1662 bp in length
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137140: contig of 34372 bp in length.
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                                                                                                                                                                                                                                                                                    Center: NIH Intramural Sequencing Center
                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
....- project Information
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/note="assembly_fragment
clone_end:T7
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/clone="RP86-117J4"
                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: awg
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                                                                                                                                                                                                                                                                                                                                        Center code: NISC
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                                                                                                                                                                                                          Green, E.D
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JOURNAL
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JOURNAL
                                                                                                                                                                                                            AUTHORS
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 147267)
Kaul, R. K., Olson, M. V., Raymond, C., Clendenning, J. and Haugen, E.D.
Direct Submission
                                                                                                                                                                                                                                                                   Treat. Submission (Control of Manual Control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: unknown; 65% of reads
Sequencing vector: plasmid; L08752; 35% of reads
Chemistry: Dye-terminator ET; 66% of reads
Chemistry: Dye-terminator ET; 66% of reads
Chemistry: Dye-terminator Big Dye; 34% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 145614 bases at least Q40
Consensus quality: 146445 bases at least Q20
Consensus quality: 146882 bases at least Q20
Insert size: 147067; sum-of-contigs
Quality coverage: 9.4x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. It currently * consists of 3 contigs. The true order of the pieces * is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 147267;
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8575: gap of unknown length
47158: contig of 38583 bp in length
47258: gap of unknown length
147267: contig of 100009 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: University of Washington Genome Center
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/clone_lib="RPCI human BAC library 11"
1. .8475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.genome.washington.edu
Contact: uwgchtgs@u.washington.edu
Drafting Center: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: chr-3 (bc0228)
Center clone name: RPI1-107K23 (bc0228)
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/note="assembly_name:Contigl3"
ture 47259. 147267. 147267 / note="assembly_name:Contigl4"
45465 a 29529 c 28742 g 43321 t
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Pred. No. 96;
0; Mismatches
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/chromosome="3"
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Best Local Similarity
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JOURNAL
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AC097356 AC024017
AC097356.1 GI:16153306
HTG; HTGS_PHASE1; HTGS_RAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
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147267 bp DNA linear HTG 16
HOMO sapiens chromosome 3 clone RP11-107K23, WORKING DRAFT
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43766 43865: gap of 100 bp
43866 47699: contig of 3834 bp in length
47700 47799: gap of 100 bp
78352 78451: gap of 100 bp
78452 81539: contig of 30552 bp in length
78452 81539: contig of 3088 bp in length
81540 88953: contig of 7314 hp in length
                                                                                                                                                                                                                                                                                                      95325 95424: gap of 100 bp
95425 98902: contig of 3478 bp in length
98903 99002: gap of 100 bp
99003 138716: contig of 39714 bp in length.
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/note="assembly_fragment:01608"
45713 a 26430 c 25963 g 39610 t 1000 others
                                                                                                                                                               contig or 100 bp contig of 7314 bp in length 100 bp contig of 7314 bp in length 100 bp contiguity
                                                                                                                                                                                                                                            88954 89053: gap of 100 bp
89054 95324: contig of 6271 bp in length
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iragment_chain:1"
2525. .24808
/note="assembly_fragment:02177
iragment_chain:1"
24909 .35362
/note="assembly_fragment:01947
iragment_chain:1"
35463 .43765
/note="assembly_fragment:00801
fragment_chain:1"
43866 .47699
/note="assembly_fragment:01909
fragment_chain:1"
47800 .78351
/note="assembly_fragment:01909
fragment_chain:1"
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fragment_chain:1"
47800 .78351
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/note="assembly_fragment:00075
fragment_chain:2"
89054 . .95324
/note="assembly_fragment:01879
fragment_chain:2"
95425. .98902
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/note="assembly_fragment:02178
fragment_chain:2"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="RP13-143F22"
/clone_lib="RPC1-13.1"
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Best Local Similarity 94.45
Matches 17; Conservative
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and coworkers at the Roswell Park Cancer Institute

NEIGHBORING SEQUENCE INFORMATION:

pBACe3.6

(http://bacpac.med.buffalo.edu)

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (08-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (08-NOV-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
5 (bases 1 to 148418)
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                                                                  PRI 09-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                           Example 2. Description of the control of the contro
                                 AC020698 148418 bp DNA linear PRI 09-M
Homo sapiens BAC clone RP11-45F23 from 5, complete sequence.
AC020698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nguyen,C., Drone,K., Hawkins,M. and Ureta,M. The sequence of Homo sapiens BAC clone RP11-45F23 Unpublished
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Contact: sapiens@watson.wustl.edu
------ Summary Statistics
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4 (bases 1 to 148418)
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Direct Submission
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The clone sequenced to the left is RP11-462622. Actual start of this clone is at base position 1 of RP11-45F23; actual end is at base position 148418 of RP11-45F23. Location/Qualifiers
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/note="similar to EST BE087288 (NID:98477683)"
                                                                         /organism="Homo sapiens"
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23355, .23440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="MER2_type"
4107. .24872
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                                                                                                                                              /clone_lib="RPCI-11"
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30287, 30727
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30745. .31216
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28790. .28843
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24873. .2520
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23485. .23625
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31227. .31275
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21287. 22345
                                                                                                                                                                                                 /rpt_family="L1"
807. 2585
/rpt_family="L1"
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1353. 11406
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.9869. .20177
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22727. .22937
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507. .807
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251. .3596
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/rpt_family="L1"
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/rpt_family="L1"
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                                                                                                        /chromosome="2"
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                                                                1. .148418
                                                                                                                    /map="5"
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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.G. and de Jong, F.G. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

MAPPING INFORMATION:

restriction digest.

SOURCE INFORMATION:

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 0); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by

This sequence was finished as follows unless otherwise noted:

repeat_region

09-APR-2000 (Rel. 63, Created) 14-MAY-2000 (Rel. 63, Last updated, Version 2)

AC036175.2

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EST AA503255 (NID:g2238222) ng77a04.s1"
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                                                                                                                                                                                                                                                                                                                   EST AA214188 (NID:91812807) zq90d03.s1"
                                                                                                                                                                                                                                                                                                                                                                                       EST A1559976 (NID:94510181) tq77e09.x1"
                                                                                                                                                                                                                                                                                                                                                                                                                        EST AA521266 (NID:92261809) aa75f02.s1"
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34414. 34495
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/note="similar to
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32104, .32229
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91.1%; Score 16.4; DB 9; Length 148418; 94.4%; Pred, No. 96; 1; Indels 0; Mismatches Db 126722 ATTCTCGGTCATGTTAA 126739 1 atactctggtcatgttaa 18 17; Conservative Matches δ

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Gaps

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standard; DNA; HTG; 164235 BP. AC036175 AC036175;

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RA Birren B., Linton L., Nusbaum C., Lander E., Abraham H., Allen N.,
RA Anderson S., Baldwin J., Barna N., Bastien V., Beda F., Boguslavkiy L.,
Boukhgalter B., Brown A., Burkett G., Campopiano A., Castle A., Choepel Y.,
RA Colangelo M., Collins S., Collymore A., Cooke P., Dearellano K., Dewar K.,
RA Diaz J.S., Dodge S., Domino M., Doyle M., Ferrelra P., Fitzhugh W.,
RA Grade D., Galagan J., Gardyna S., Ginde S., Goyette M., Graham L.,
RA Grand-Pierre N., Grant G., Hagos B., Heaford A., Horton L., Howland J.C.,
RA Lamazares R., Landers T., Leflors A., Klein J., LaRoque K.,
RA Locke K., Macdonald P., Marquis N., Mercarthy M., McEwan P., McGurk A.,
RA McKernan K., McPheeters R., Meldrim J., Meneus L., Mihova T., Mirahy T., Naylor J., Norman C.H., O'Connor T.,
RA Mienga V., Morrow J., Murphy T., Naylor J., Norman C.H., O'Connor T.,
RA Pisani C., Pollara V., Raymond C., Riley R., Rogov P., Rothman D., Roy A.,
RA Santos R., Schauer S., Severy P., Spencer B., Stange Thoman N.,
Stojanovic N., Subramanian A., Talamas J., Tesfaye S., Theodore J.,
RA Wilson B., Wu X., Wyman D., Ye W.J., Young G., Zainoun J., Zimmer A.,
                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                          Homo sapiens chromosome 2 clone RP11-704A16 map 2, WORKING DRAFT SEQUENCE, 19 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (07-APR-2000) to the EMBL/GenBank/DDBJ databases. Whitehead Institute/MIT Center for Genome Research, 320 Charles Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On May 12, 2000 this sequence version replaced gi:7523843.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. It currently * consists of 19 contigs. The true order of the pieces * is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality coverage: 4.5 in 020 bases; agarose-fp Quality coverage: 4.7 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 155591 bases at least Q40 Consensus quality: 159816 bases at least Q20 Consensus quality: 161495 bases at least Q20
                                                                                                                                                                                                                                                                             1-164235
Birren B., Linton L., Nusbaum C., Lander E.;
"Homo sapiens chromosome 2, clone RP11-704A16";
Unpublished.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: WIBR
Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 168000; agarose-fp
Insert size: 162435; sum-of-contigs
                                                                                                                                                 HTG; HTGS_DRAFT; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --- Genome Center
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                                                                                                                                                                                  Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                           1-164235
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Submitted (24-JAN-2002) Genome Sequencing Center, Washington Submitted (24-JAN-2002) of Medicine, 4444 Forest Park Parkway, St. Louis, University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA On Jan 26, 2002 this sequence version replaced gi:18308946.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166922 bp DNA linear HTG 26-JAN-2002 Homo sapiens chromosome 2 clone RP11-704A16, WORKING DRAFT SEQUENCE, 2 unordered pieces.
                                                                                                                                  7827. .66313

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66414. .78356

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78457. .90502

/note="assembly_fragment"

90603. .110197

/note="assembly_fragment"

110298. .132734

/note="assembly_fragment"
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 164235 BP; 52554 A; 29032 C; 29120 G; 51728 T; 1801 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.18; Score 16.4; DB 30; Length 164235; 94.48; Pred. No. 96; trive 0; Mismatches 1; Indels 0; trive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Washington University Genome Sequencing Center
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Sequencing vector: plasmid; 57%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-primer B1; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consenby program: Phrap; version 0.990319
Consensus quality: 166298 bases at least Q30
Consensus quality: 166729 bases at least Q20
Insert size: 168000; agarose-fp
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AC108072.2 GI:18376983
HTG; HTGS_PHASE1; HTGS_ACTIVEFIN.
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/note="assembly_fragment"
39540. .47837
/note="assembly_fragment"
47938. .58126
                                                                                      47938. .58126
/note="assembly_fragment"
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Waterston, R.H.
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Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
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SX
XX
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          * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                                                         110; gap of 100 bp 1055; contig of 3849 bp in length 1055; gap of 100 bp 15310; contig of 4251 bp in length 5410; gap of 100 bp 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110198 110297; gap of 100 bp
110298 113734; contig of 22437 bp in length
132735 132834; gap of 100 bp
132835 164235; contig of 31401 bp in length.
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39439: contig of 7021 bp in length
39539: gap of 100 bp
47837: contig of 8298 bp in length
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32318: contig of 5604 bp in length
                                                                                                                                                                                                                                                                                          of 100 bp contig of 1826 bp in length
                                                                                                                                                                                                                                                                                                                                           of 100 bp
contig of 2304 bp in length
                                                                                                                                                                                                                                            of 100 bp
contig of 1274 bp in length
                                                                                                                                                                1026: contig of 1026 bp in length
                                                                                                                                                                                      of 100 bp contig of 180 bp in length
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1111. .10959
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'note="assembly_fragment"
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78356: cont
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58126: cont
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110197: con
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1407 2680; cor
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4606: co
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1127 1306: co
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7010: co
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Submitted (05-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requeststeanger.ac.uk
On Sep 6, 2001 this sequence version replaced gi:14272282.
During sequence assembly data is compared from overlapping clones.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 176355)
Laird,G.
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                                                                                                                                                                                       arbitrary daps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL356053 176355 bp DNA linear PRI 05-
Human DNA sequence from clone RP11-453G10 on chromosome 10,
                                                                                                           * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.1%; Score 16.4; DB 2; Length 166922; 94.4%; Pred. No. 96; Live 0; Mismatches 1; Indels 0;
Insert size: 166822; sum-of-contigs
Quality coverage: 11.20 in Q20 bases; agarose-fp
Quality coverage: 11.28 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                 1 1113: contig of 1113 bp in length 1213: gap of unknown length 4 166922: contig of 165709 bp in length. 1.166922
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/note="assembly_name:Contig8
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54810 a 30046 c 29856 g 52110 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'clone="RP11-704A16"
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in the feature table with their source databases: Em:, EMBL; Sw:, datSpsRoyT Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence thttp://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr10 can be found at RPI1-453G10 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                        IMPORTANT: This sequence is not the entire insert of clone RPI1-453G10 It may be shorter because we sequence overlapping sections only once, except for a short overlap.
The true right end of clone RPI1-453G10 is at 176355 in this sequence. The true right end of clone RPI1-19501 is at 100 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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/note="match: GSS: En: A0149763"
complement(101941. .102380)
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164173. ,164612
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Matches 17; Conservative
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Search completed: July 31, 2002, 14:02:35 Job time: 17597 sec

us-09-899-718a-8.rge

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

July 31, 2002, 12:23:49; Search time 165.21 Seconds (without alignments) 35.683 Million cell updates/sec Run on:

US-09-899-718A-7 24

1 tcagccagttccaccccgtgcacg Perfect score: Sequence:

IDENTITY_NUC Gapox 1.0 Scoring table:

383533 seqs, 122816752 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%.
Maximum Match 100%
Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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SUMMARIES		ΩI	US-09-060-756-461	-457-9	US-08-385-370-1	US-08-385-370-3	118-08-303-37-3	US-08-060-410-3	US-09-060-156-567	US-08-611-107-1	US-08-422-5604-1	US-08-468-793-1	IIS-08-581-148C-15	US-07-903-029-2	118-09-155-769-1	TIS-00-103-040%-0	TR-09-103-9408-1	T-WO-303-E0E-1	7-007-707-70	US-U9-33U-611-11	T=QT8-7//3-8TP-T	US-U9-29/-93/C-8	US-09-297-937C-12	US-08-998-416-307	US-08-212-190A-1	US-08-900-321-1	PCT-US95-03610-1	US-08-619-542B-29	72-2	115-08-901-306-3	1
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US-09-180-271-3 US-09-049-672A-21 US-09-199-673A-135 US-09-199-673A-135 US-08-889-402-3 US-08-889-402-6 US-08-889-402-6 US-08-889-402-6 US-08-889-402-6 US-08-889-402-6 US-07-928-464-1 US-08-261-432-1 US-07-928-464-3 US-07-928-464-3 US-07-928-464-3 US-07-928-464-3 US-07-928-464-5 US-07-928-464-5 US-07-928-464-5
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ALIGNMENTS

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060756 Roland ISOLA OF A PLICAT /09/06 6	within are u	Score 17.6; Pred. No. 51; 0; Mismatches g 24 f 1 G 29
SEULT 1 Sequence 461, Application US/09060756 Sequence 461, Application US/09060756 Patent No. 6183957 APPLICANT: Cole, Stewart APPLICANT: Cole, Stewart APPLICANT: Buchrieser-Brosch, Roland APPLICANT: Buchrieser-Brosch, Roland APPLICANT: Buchrieser-Brosch, Roland APPLICANT: Bullault, Alain TITLE OF INVENTION: METHOD FOR ISOLATING TITLE OF INVENTION: LIBRARY APPLICATION THE GENOME OF A MYCOB FILE REFERENCE: 3495-0169 CURRENT APPLICATION NUMBER: US/09/060,756 CURRENT FILING DATE: 1998-04-16 NUMBER OF SEQ ID NOS: 743 SEQ ID NO 461 LENGTH: 114 OFFATH: 114 OFFATH: NA	positions within the sequence) applicants are uncertain of bases designated	38; 38; 38; JCAC
cation tewart ser-Br Steph t, Ala t,	s posi	ry 8 ervativ
Appli 83957 MATION MATION Corpor, Sordon, Sord	NAME/KEY: unsure LOCATION: (various OTHER INFORMATION: 9-060-756-461	th Similarity 83 20; Conservative agccagttccaccccgtc
1756-4 9 461, NO. 611, NO. 611	NAME/KEY: unsure LOCATION: (vario OTHER INFORMATIO 9-060-756-461	tch 20; tcagcc 1
RESULT 1 Sequence 461, Application US Patent No. 6183957 GENERAL INFORMATION: APPLICANT: Cole, Stewart APPLICANT: Buchrieser-Brosc APPLICANT: Gordon, Stephen TITLE OF INVENTION: MATHOD TITLE OF INVENTION: MATHOD TITLE OF INVENTION: METHOD TITLE OF INVENTION: ALBAN TITLE OF INVENTION: LIBRARY FILE REFERENCE: 3495-0169 CURRENT PELLING DATE: 1998-0, NUMBER OF SEQ ID NOS: 743 SOFWARE: PATENTIN OF 120 NUMBER OF SEQ ID NOS: 743 SOFWARE: PATENTIN OF 120 SEQ ID NO 461 LENGTH: 114 TYPE: DNA ORGANISM: MYCODACTETIUM tul	; NAME/KEY: unsure LOCATION: (various ; OTHER INFORMATION: US-09-060-756-461	Query Match Best Local Similarity Matches 20; Conser 1 tcagccagttccac
RESULT US-09- Sequ- Sequ- Repair APP APP TITT TITT TITT TITT TITT TITT T	; ; us-0	Qu Bee Ma Qy Db

RESULT 2
US-09-437-457-8/C
US-09-437-457-8/C
Sequence 8, Application US/09437457
Sequence 8, Application US/09437457
Sequence 8, Application US/09437457
Sequence 9, Application US/09437457
Sequence 9, Application Sequence 1 Sequence 1 Sequence 1 Sequence 2 Sequenc

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APPLICANT: Vainio, Arja
APPLICANT: Vainio, Arja
APPLICANT: Pagerstrom, Richard
APPLICANT: Rorhola, Matti
APPLICANT: Rorhola, Matti
APPLICANT: Norhola, Matti
APPLICANT: Norhalainen, Helena
TITLE OF INVENTION: Limit Dextrinase Activity in Trichoderma
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/385,370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Sterne, Kessler, Goldstein & Fox 1100 New York Ave., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0270004
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 2040 TCCGCCAGCTCCACCCGGGCA 2061
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                                                                                                                                                                 ; Sequence 3, Application US/08385370 ; Patent No. 5665585
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TELERAX: (202) 371-2540
TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                    APPLICANT: Torkkeli, Tuula
APPLICANT: Joutsjoki, Vesa
APPLICANT: Torkkeli, Helena
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                             US-08-385-370-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Torkkeli, Tuula
APPLICANT: Torkkeli, Helena
APPLICANT: Torkkeli, Helena
APPLICANT: Torkkeli, Helena
APPLICANT: Torkkeli, Helena
APPLICANT: Fagerstrom, Richard
APPLICANT: Forfola, Matti
APPLICANT: Korfola, Matti
APPLICANT: Nevalainen, Helena
APPLICANT: Forfola, Matti
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                                                                                                                                                                                                Query Match
71.7%; Score 17.2; DB 4; Length 230;
Best Local Similarity 86.4%; Pred. No. 75;
Matches 19; Conservative 0; Mismatches 3; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Ave., Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.7%; Score 17.2; D
86.4%; Pred. No. 76;
tive 0; Mismatches
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NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/385,370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08385370 Patent No. 5665585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                  2 cagccagttccacccgtgcac 23
                                                                                                                                                                                                                                                                                                                                                42 CTGCCAGTTCCAGCCCGTGCTC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 371-2540
TELEX: 248636 SSK
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (202) 371-2600
(202) 371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Cimbala, Michele A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEGETH: 1996 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 86.4
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
                                                                                                                     ; ORGANISM: Homo sapiens US-09-437-457-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: both US-08-385-370-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.0
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                                                                          LENGTH: 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-385-370-1
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                                                                                                  TYPE: DNA
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                                                                        Query Match 71.7%; Score 17.2; DB 1; Length 2745; Best Local Similarity 86.4%; Pred. No. 76; Matches 19; Conservative 0; Mismatches ?
; LOCATION: join(295..520, 594..898, 1075..1583, 1637..2447)
US-08-385-370-3
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Gaps
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ZAMB, TIMOTHY
APPLICANT: LIANG, XIAOPING
APPLICANT: BABIUK, LORNE A.
TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE I
TITLE OF INVENTION: VACCINES
NUMBER OF SEQUENCES: 21
CORRESPONDENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITT: Pala Alto
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09060410
Patent No. 6165461
GENERAL INFORMATION:
APPLICANT: Cobb, Melanie
APPLICANT: Hutchinson, Michele
APPLICANT: Chen, Zhu
APPLICANT: Chen, Zhu
APPLICANT: Chen, Zhu
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,861
FILING DATE: 09-SEP-1994
CLASSIPICATION: 435
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STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSAFLACTURN: 43.0

ATORNEY/AGENT INFORMATION:
NAME: PARK, FREDDIE K.
REGISTRATION NUMBER: 35,636
REFERENCE/DOCKET NUMBER: 29310-20020.20
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 494-0792
TELEPRA: (415) 494-0792
TELEPRA: (415) 494-0792
TELEPRA: (415) 498-0792
SEQUENCE CHARACTERISTICS:
LENGTH: 1788 base pairs
TYPE: nucleic acid
STAPE: nucleic acid
STAPE: nucleic acid
STAPE: nucleic acid
STAPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                         ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 cagccagttccaccccgtgc 21
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STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: 97..
US-08-303-861-1
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APPLICANT: Cole, Stewart
APPLICANT: Cole, Stewart
APPLICANT: Buchir-ser-Brosch, Roland
APPLICANT: Gordon, Stephen
TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLECTIDE OF INTEREST FROM
TITLE OF INVENTION: HER GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
FILLE REFRENCE: 3495-016
CURRENT APPLICATION NUMBER: US/09/060,756
CURRENT FILING DATE: 1998-04-16
NOWBER OF SEQ ID NOS: 743
SOWMER: PARTENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (various positions within the sequence); OTHER INFORMATION: applicants are uncertain of bases designated as "n" US-09-060-756-567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060.410
                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUBER: 31,392
REFERENCE/DOCKET NUBER: 860098.421
TELECOMMUNICATION INFORMATION:
TELEPAX: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4296 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                 UMBER: US/09/060,410
14-APR-1998
                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 567, Application US/09060756
; Patent No. 6183957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 tcagccagttccaccccgtgcacg 24
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  Floppy disk
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Best Local Similarity 90.0 Matches 18; Conservative
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Best Local Similarity 79.29
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 193..3171
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                                                                                                                                  FILING DATE: 1. CLASSIFICATION:
MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure
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LENGTH: 374
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P.O. Box 4433

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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
TITLE OF INVENTION: ACETYL-COA CARBOXXLASE COMPOSITIONS AND
TITLE OF INVENTION: METHODS FOR USE
                                                                                                      APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS ENCODING
TITLE OF INVENTION: ACETYL-COA CARBOXYLASE AND USES
TITLE OF INVENTION: THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,107 FILING DATE: CONCURRENTHY Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION 800
PRIOR APPLICATION BATA:
APPLICATION NUMBER: US SN 07/956,700
FILING DATE: 02-0CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/09340
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US PCT/US93/09340
APPLICATION NUMBER: US SN 08/422,560
APPLICATION NUMBER: US NO 8/422,560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US SN 08/422,560 FILING DATE: 14-APR-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD:221
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                               ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston
                                                                                                                                                                                                                                                                                                                                                              United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 1, Application US/08422560A; Patent No. 5910626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               387 TTAGCCAGTTCCACCTCTAGCAC 365
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                                      Sequence 1, Application US/08611107
Patent No. 5801233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1458 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, W
                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
US-08-611-107-1
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                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     Texas
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                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: Ur
RESULT 8
US-08-611-107-1/c
                                                                                                                                                                                                                                                                                                                                                  STATE:
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Gaps
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APPLICANT: Gornicki, Piotr
TITLE OF INVENTION: ACETYL-COA CARBOXYLASE COMPOSITIONS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 69.2%; Score 16.6; DB 2; Length 1458; Best Local Similarity 82.6%; Pred. No. 1.3e+02; Matches 19; Conservative 0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/422,560A FILING DATE: 14-APR-1995 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/422,560
FILING DATE: 14-APR-1995
APPLICATION NUMBER: US SN 07/956,700
FILING DATE: 02-0CT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                     ARCD: 152/WIM
                                                                                                                                                                                                                                                                                                CLASSIFLCATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/956,700
FILING DATE: 02-001-1992
ATTORNEY AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REPRENCE/DOCKET NUMBER: ARCD:152/WI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRERY APPLICATION DATA:
APPLICATION NUMBER: US/08/468,793
FILING DATE: 06-JUN-1995
FILING DATE: 08-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Texas COUNTRY: United States of America ZIP: 77210
                                                                                                                                                 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-468-793-1/c; Sequence 1, Application US/08468793; Patent No. 6177267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       387 TTAGCCAGTTCCACCTCTAGCAC 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 tcagccagttccacccgtgcac 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 512-47-777
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENOTH: 1458 base pairs
                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                     77210-4433
STREET: P.U. P.TTV: Houston
                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-422-560A-1
                                                                                                                                                          COMPUTER:
                                                                     COUNTRY:
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us-09-899-718a-7.rni

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ATTORNEY/AGENT INFORMATION:
NAME: Benett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: 07-21(872)A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
BEDIUM TYPE: Floppy disk
CMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                      266 TCAGCCGGTACCACTCCTTGCAC 288
                                                                                                                                                                                                                                                               1 tcagccagttccaccccgtgcac 23
               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     500 TCACCCAGTICCTCCCCGGGC 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (314)694-5402
TELEPAX: (314)694-9009
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                             Query Match
Best Local Similarity 82.68
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 589 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85.74
Matches 18; Conservative
                                                                                                1..1665
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US-07-903-029-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              St. Louis
Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                           ; NAME/KEY: CDS
; LOCATION: 1..1
US-08-581-148C-15
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US-07-903-029-2/C
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US-09-155-768-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Schable, Patrick S.
APPLICANT: Robertson, Donald S.
APPLICANT: Hansen, Joel D.
APPLICANT: Nikolau, Basil J.
APPLICANT: Xia, Xiaojie
APPLICANT: Xia, Xiji
TITLE OF INVENTION: ISOLATION AND USE OF CUTICULAR LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,148C
FILING DATE: 29-DEC-1995
CLASSIFICATION: 800
                                                                CLEASLIFLEATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD:152/KIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: 79-0324
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 1458 base pairs
TYPE: nucleic acid
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
            APPLICATION NUMBER: PCT/US93/09340
FILING DATE: 30-SEP-1993
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                 : IUPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-468-793-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15, Application US/08581148C Patent No. 6060644 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Larcher, Carol
REGISTRATION NUMBER: 35243
REFERENCE/DOCKET NUMBER: 7138(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 tcagccagttccaccccgtgcac 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1903 base pairs
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 60601-6780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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Gaps
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0
69.2%; Score 16.6; DB 3; Length 1903; 82.6%; Pred. No. 1.3e+02; tive 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                Sequence 2, Application US/07903029
Patent No. 5969097
GENERAL INFORMATION:
APPLICANT: Wlegand, Roger C.
APPLICANT: Currie, Mark C.
APPLICANT: Fow, Kam F.
TILLE OF INVENTION: Human Guanylin
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bonnis A. Bennett, Monsanto Co., A3SG
STREET: 800 N. Lindbergh Blvd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903,029
FILING DATE: 19920623
ATTORNEY: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.5%; Score 16.2; DB 2;
85.7%; Pred. No. 1.9e+02;
tive 0; Mismatches 3;
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LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                SEC ID NO 1
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OTHER INFORMATION: "n" bases at various positions throughout the sequence
COTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: PRASER, Claire M.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT PILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PALENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 67.5%; Score 16.2; DB 4; Length 4403765; Best Local Similarity 90.0%; Pred. No. 54; Matches 18; Conservative 0; Mismatches 2; Indels 0; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 67.5%; Score 16.2; DB 4; Length 2117; Best Local Similarity 85.7%; Pred. No. 1.9e+02; Matches 18; Conservative 0; Mismatches 3; Indels 0;
                                AFFLICANT: SLINDARN CONCURS. CONTRACTOR TYPIES OF TITLE OF INVENTION: POLYPEPTIDE OF HYALURONAM SYNTHASE OF TITLE OF INVENTION: HUMAN-ORIGIN AND DNA ENCODING THE SAME FILE REFERENCE: TOYAM37.001APC
CURRENT APPLICATION NUMBER: US/09/155,768A
CURRENT PELLING DATE: 1996-10-05
EARLIER PELLING DATE: 1996-04-05
EARLIER PLIING DATE: 1996-04-30
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FRAELER FILING DATE: 1996-04-30
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 2098669 CACCCAGTTCCACCGGTGC 2098650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      % OS-09-103-840A-2/C

% Sequence 2, Application US/09103840A

% Patent No. 6294328

GENERAL INFORMATION:

APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 1374 GCCAGTGCCACGCCTGCACG 1354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 gecagitecaccecgigeacg 24
GENERAL INFORMATION:
APPLICANT: SEIKAGAKU CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 cagccagttccaccccgtgc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , LOCATION: (149)...(1777)
US-09-155-768-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4403765
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US-09-103-840A-1/C
                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                           2117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
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APPLICANT: FIRESCHAMA, Robert D.
APPLICANT: WITTE, OWER R.
APPLICANT: WITTE, OWEN R.
APPLICANT: FRESR, Claire M.
APPLICANT: FRESR, Claire M.
APPLICANT: VERESR, Claire M.
TITLE OF INVENTION: JOHN C.
TITLE OF INVENTION: JUBECULOSIS
FILE REPERMER: 2.466-2007,00
CHIREN FILEND ADTE: 1999-06.24
NUMBER OF SEO ID NOS: 2
SEOTION D. APPLICATION WINER: US/09/103,840A
NUMBER OF SEO ID NOS: 2
SEOTION M.
SEO ID NOS: 2
OUGENIEW FILEND ADTE: 1999-06.24
SEOTION M.
SEO ID NOS: 3
OUMER WATCH A11259
TTPE: DOIS-SHOAL
SEO ID NOS: 2
SEOTION M.
SEO ID NOS: 3
OUMER WATCH A11259
TTPE: DOIS-SHOAL
SEO ID NOS: 2
SEOTION M.
SEO ID NOS: 3
MARCHAE MAINTENDENTIAL M.
SEO ID NOS: 3
TTPE: DOIS-SHOAL
MATCHAE MAINTENDENTIAL M.
SEO ID NOS: 3
TTPE: DOIS-SHOAL
MATCHAE MAINTENDENTIAL M.
SEO ID NOS: 3
TTPE: DOIS-SHOAL
MATCHAE MAINTENDENTIAL M.
SEO ID NOS: 3
TTPE: MAINTENDENTIAL M.
SEO ID NOS: 3
TTPE: DOIS-SHOAL
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Page 1

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

July 31, 2002, 12:12:09; Search time 5855.71 Seconds (Without alignments) 55.318 Million cell updates/sec Run on:

US-09-899-718A-7 24 1 tcagccagttccacccgtgcacg 24

Title: Perfect score: Sequence:

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched:

27472414 Total number of hits satisfying chosen parameters:

13736207 seqs, 6748477542 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST:* Database :

em_gss_hum:*
em_gss_inv:*
em_gss_pln:*
em_gss_vrt:* em_estba:*
em_esthum:*
em_estin:*
em_estin:*
em_estin:*
em_estpl:*
em_estpl:*
em_estpl:*
em_estpl:*
gb_estl:*
gb_estl:*
gb_htc:*
gb_htc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	0004E KO 0014A100	AT 200105 GA EQUUZ	C10EOF C10EOF DE	ATTOREAGE ATTOREAGE	AU065403 AU065405	D1610000 D1110000	B1700/188 B81/00/28	B69813/3 CM4-CN008			BG827582 602748468	BI329586 602984002	BH045197 RPCT-24-3		•	_	AZ875573 2M0190G02	BF739541 NCM10C12T	AZ831095 2M0110112
SUMMARIES		ID	BG444193	CNSO4FCX	C19505	AU065405	AU065404	BT510068	BG981373	AT162401	Ç		BG82/582	BI329586	BH045197	BG104185	AK009013	A 9 9 7 5 5 7 3	0/00/0000	BF / 3954 I	AZ831095
		DB	10	12	10	σ	σ	10	10	σ	, -	1 5	10	07	12	10	-	1,5	1 -) i	12
		Match Length DB	836	808	420	453	460	306	426	52R	1 1	000	100	707	765	907	1200	24		* *	249
dР	Query	Match	80.8	80.0	78.3	78.3	78.3	75.8	75.8	75.8	75.8	0 0	0.0	70.0	8.07	75.8	75.8	74.2	2,47	1 .	7.4/
		Score	19.4	19.2	18.8	18.8	18.8	18.2	18.2	18.2	18.0	100	7 C	7.07	7.07	18.2	18.2	17.8	17.8	27.0	17.0
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DEFINITION

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KEYWORDS

SOURCE

CNS04FCX/C

ORGANISM

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REFERENCE

AUTHORS

JOURNAL REFERENCE

TITLE

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I (bases 1 to 453)
Minobe, Y. and Sasaki, T.
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AU065405 Rice root Oryza sativa cDNA clone R3592_1A, mRNA sequence.
420 bp mRNA linear EST 24-OCT-1996 C19505 Rice panicle at ripening stage Oryza sativa cDNA clone ELIOSZ_1A, mRNA sequence.
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Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
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Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/.
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Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
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/db_xref="taxon:4530"
/clone="E10525_1A"
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Fax: 81-298-38-7468
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
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Roset-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Roset-Crollius, H., Wincker, P., Brottler, P., Quetier, F., Saurin, W. and Weissenbach, J. ..., Sauring with analysis insing
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                                                                                                                                         80.8%; Score 19.4; DB 10; Length 836; 95.2%; Pred. No. 8.6e+02; tive 0; Mismatches 1; Indels 0,
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/clone="106E04"
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BB170026B10G05 Bee Brain Normalized/Subtracted Library, BB17 Apis
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1 (bases 1 to 460)
Minobe, Y. and Sasaki, T.
Rice ophyta; Embryophyta; Tracheophyta; Entractions of the form root.
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Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 81-298-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
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Pred. No. 1.3e+03;
/strain="Nipponbare, sub_species Japonica"
/db_xref="taxon:4530"
                        /db_Are._______/clone="18592_lA"
/clone="18592_lA"
/clone_lib="Rice root"
/note="Prepared from seedling root."
176 a 84 t 4 others
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/dxxref="taxon:4530"

/clone="R3590_lA"

/clone="Rice root"

/note="Prepared from seedling root."
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                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa.
                                                                                                                                             Query Match
Best Local Similarity
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505 S. Goodwin Ave., Urbana, IL 61801, USA
Tel: 217 265 0309
Fax: 217 244 3499
Email: generobielife.uiuc.edu
This research was funded by the University of Illinois Critical
Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
Award in Functional Genomics to G.E. Robinson and an NSF
Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
                     Pterygota; Neoptera; Endopterygota; Harapoda; Insecta; Apoidea; Apidae; Apis.
Apoidea; Apidae; Apis.
I (bases 1 to 306)
Whitfield, C.W., Soares, B., Robertson, H.M., Pardinas, J., Liu, L., An Expressed Sequence Tag Resource for Studies of Brain and Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anote—"Organ: Drain; Vector: pT7T3-Pac; Site_1: EcoR1; Site_2: Not1; This BB17 cDNA library was generated by subtraction of the BB16 library with 4000 previously sequenced clones. The BB16 library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6 (9): 791-806. RNA was prepared from dissected brains of adult worker bees of various ages and various behavioral groups. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Apis mellifera"
/strain="mixed strains of European bees, predominantly
A.m. ligustica "
/db_xref="taxon:7460"
/clone="Ball70026810G05"
/clone=lib="Bee Brain Normalized/Subtracted Library, BB17"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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СМ4-CN0089-070201-746-e01 CN0089 Homo sapiens cDNA, mRNA sequence.
BG981373
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Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 426)
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 2.2e+03;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="brain"
/dev_stage="adult worker honey bee"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR PRIMERS
FORWARD: TAATACCACTCACTATAGGG
BACKWARD: ATTAACCCTCACTAAAG
Insert Length: 306 Std Error: 0.00
Plate: BB170026B10 row: G column: 0:
Seq primer: AGCGGATAACAATTCAACAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 306.
Location/Qualifiers
                                                                                                                                                                                                                            Contact: Gene E. Robinson
Department of Entomology
University of Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 TCGCCAGTTCCACCCCGTGCTC 278
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87.0%;
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Matches 20; Conservative
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KEYWORDS
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Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18
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Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreld, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 02-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBluescript SK; Site_1: Sal1: Site_2: Not1; Cambial region tissues, including developing xylem, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   meristematic cambial zone and the developing and mature phloem, was harvested from 1.5 m actively growing trees. CDNA was prepared and cloned into lambda g122a. DNA was isolated and subcloned into pBluescript SK using SalI and NoII restriction enzymes." 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                  /organism="Populus tremula x Populus tremuloides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.8%; Score 18.2; DB 9; Length 528; 87.0%; Pred. No. 2.3e+03;
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239242 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Hybrid aspen plasmid library"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Cambial region"
/dev_stage="1.5 m actively growing tree"
/lab_host="E.coli"
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Fax: 402 762 4390
Contact: Sterky F
Department of Biotechnology
Royal Institute of Technology (KTH)
Teknikringen 34, S-100 44 STOCKHOLM, Sweden
Tel: +46 8 790 8287
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PO Box 166, Clay Center, NE 68933-0166, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                               FORWARD: AAAGGGGGATGTGCTGCAAGGGG
BACKWARD: GCTTCCGGCTGCTATGTTGTGTG
Seq primer: GGTTGTAAAAGGAGGCCAG
High quality sequence stop: 528.
Location/Qualifiers
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Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:47664"
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                                                                                                                                                                fredrik@biochem.kth.se
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Matches 20; Conservative
                                                                                                                                        Fax: +46 8 24 54 52
                                                                                                                                                                                                    PCR PRimers
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Gene discovery in the wood-forming tissues of poplar: Analysis of 5,692 expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 95 (22), 13330-13335 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: colon_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES POR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear EST 03-DEC-1998
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Populus tremula x Populus tremuloides
Populus tremula x Populus tremuloides
Bukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosides; eurosids 1; Malpighiales; Salicaceae; Populus.
                                      Dias Neto, E., García Correa, R., Verjovskí Almeida, S., briones, P. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Nagai, M. A., de arvalho, R.F., Matsukuma, A., Bala, G. S., Simpson, D. H., Brunstein, A., deolivelra, P. S., Bucher, P., Jongeneel, C. V., O' Hare, W. J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S. J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4&t2=CM4-CN0089-070201-746=e01&t3=2001-02-07&t4=1)
Seq primer: puc 18 forward
                        Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
                                                                                                                                                                                                                                                                                                              Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A018P38U Hybrid aspen plasmid library Populus tremula x Populus
                                                                                                                                                                              Shorgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                       Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'organism="Homo sapiens"
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High quality sequence stop: 426.
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/dev_stage="Adult"
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                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
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Best Local Similarity 87.09
Matches 20; Conservative
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B1329586 702 bp mRNA linear EST 30-JUL-2001 602984002F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5136697 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 70%)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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RPCI-24-301рэ.TV RPCI-24 Mus musculus genomic clone RPCI-24-301рэ,
DNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 765)
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/ Ob_ratel="ryb,"
/ Clone="IMAGE:5136697"
/ Clone="IMAGE:5136697"
/ Lab_host="Nation CGAP_Li19"
/ Ab_host="Organ: liver, Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally, Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."
a 237 c 204 g 131 t
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI336 row: c column: 02
High quality sequence stop: 533.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/strain="FVB/N"
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                   1 tcagccagttccaccccgtgcac 23
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/db_xxef="taxon:9606"
/clone="InAge=1401416"
/clone_ilb="NIH_MGC_17"
/tissue_type="Thabdomyosarcoma"
/lab_host="blind (phage-resistant)"
/note="Organ: muscle; Vector: poTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAGG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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50274846881 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4901416 5',
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NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                 /note="Vector: pCMV SPORT6; Site_1: xbal; Site_2: xhol; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."
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CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM1796 row: g column: 17
High quality sequence start: 4
High quality sequence start: 4
High quality sequence stop: 551.
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Pest Local Similarity 87.0%; Pred. No. 2.46+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
/organism="Sus scrofa"
                           /db_xref="taxon:9823"
/clone_lib="MARC 2PIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                687 bp
                                                                    /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                  269 TCAGCCAGATCCACCCCATGGAC 291
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Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E.,

AUTHORS

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Matches

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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                  /clone="IMAGE:4422900"
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Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library RPCI-24. For BAC
Library availability, please contact Pieter de Jong
Library availability, please contact Pieter de Jong
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 301 row: P column: 3
Seq primer: T7
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other_GSSs: RPCI-24-30IP3.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
791: 301 838 0200
Fax: 301 838 0208
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/cell_type="Spleen/Brain"
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Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:10090"
/clone="RPCI-24-301P3"
/clone_lib="RPCI-24"
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/clone_limal.yazzoo
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/lab.host="melanotic melanoma" .
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/note="Organ: skin: Vector: poTB7; Site_1: XhoI; Site_2:
/cloned into EcoRI/XhoI sites using the following 's
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZaP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
46 a 275 c 339 g 147 t
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mus musculus adult male tongue cDNA, RIKEN full-length enriched
library, clone:2300002M23:hypothetical protein, full insert
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
S (bases 1 to 1200)
Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
Carninot,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
Hume,D., Imotani,R., Ishi,Y., Itch,M., Izawa,M., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S.,
Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
Schriml,L., Shibata,R., Shibata,Y., Shi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Encyclopedia Project of Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse Lissues. First strand CDNA was primed with a primer prepare mouse Lissues. First strand CDNA was primed with a primer prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second Strand CDNA was prepared with the primer adapter of Sequence [5, WICH ANDI and SSTI. Cloning sites, 5, end: XhoI; 3, end: SSTI.
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1. .1200
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2M0190G02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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75.8%; Score 18.2; DB 11; Length 1200;
Best Local Similarity 87.0%; Pred. No. 2.6e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0;
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Direct Submission
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                                                                                                                              AUTHORS
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.00 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114)pblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
                   Mus musculus Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 64)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Kose, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: PwD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                                                                                                                                                                                                                                                                          Mouse whole genome scaffolding with paired end reads from 10kb
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Seq primer: CGTTGTAAAACGACGGCCAGT
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                                                                                                                                                                                                                                                                                                    plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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/db_xref="taxon:10090"
/clone="UUGC2M0190G02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Errc
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Fax: 801 585 7177
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Matches 19; Conserv
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

July 31, 2002, 14:11:24; Search time 720.8 Seconds (without alignments) 57.167 Million cell updates/sec Run on:

US-09-899-718A-7 Title: Perfect score:

1 teagecagttecacceegtgeacg 24 Sednence:

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

1736436 seqs, 858457221 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Cardiac sodium cha	Cardiac sodium cha	Hepatitis C virus	Drosophila melanog	Human beta-2 adren	Rat proteosome RIN	Reference sequence	DNA encoding novel	cDNA encoding gluc	
SUMMAKIES			QI	1 AAQ05831	5 AAQ81328	5 AAQ73770	23 ABL24072		5 AAQ54681	4 AAS19511	23 AAS91810	8 AAT90830	
			e Match Length DB ID	7555 1.			4541	230			1972		
	æ	Query	Match	75.8									
			Score	18.2	18.2	17.6	17.4	17.2	17.2	17.2	17.2	17.2	
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Human beta2-adrene Human beta2 adrene Glucoamylase P gen Human beta2-adren Human beta1-adrener Reference sequence DNA encoding novel Polynucleotide seq Human braast cell Human brain expressiuman bone marrow Probe #13079 used Probe #13079 used Probe #13791 used FEST clone DD401.	#762 fo brain e bone ma #788 fo
AAX61116 AAA38340 AAA38340 AAY90631 AAZ00774 AAZ00776 AAZ00776 AAZ00778 AAZ00778 AAZ00778 AAZ00778 AAZ89484 AAA3839484 AAX89475 AAA3839484 AAX20515 AAX30515	ABA22296 AAK00770 AAK26222 AAI10855
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100.88	
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ALIGNMENTS

AAQ05831 standard; cDNA; 7555 BP. Cardiac sodium channel gene 90WO-0S00768 89US-0310330 (first entry) (ARCH-) ARCH DEV CORP. Rat; arrhythmia; ss Rattus rattus. 09-FEB-1990; 13-FEB-1989; 10-JAN-1991 WO9009391-A. 23-AUG-1990 Rogart RB; AAQ05831; RESULT

New rat cardiac sodium channel proteins - and associated DNA sequences, polypeptides and peptides associated with proteins, useful as antiarrythmic and cardiotonic drugs. P-PSDB; AAR06584.

WPI; 1990-275095/36.

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94GB-0000263.
                                                                                                                                                                                                                                                                                                                                                                                                            94WO-GB00957.
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                                                             Best_Local Similarity 87.0 Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pike IH, Simmonds P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1994-358278/44.
                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus.
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                                                 Query Match
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                                                                                                                                                                            AAQ73770/c
                                                                                                                                                                 RESULT
                                                                                                  QΥ
                                                                                                                                                                                                                                                      projaryote/eukaryote host cell, and the resulting recombinant sodium channel protein has various therapeutic, diagnostic and prognostic uses. It may also be used to develop more effective antiarrythmic, cardiant and cardioglycoside drugs.
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                antiarrythmic; cardiant; cardioglycoside; pRH3-1; pRH4-23; pRH14-31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The CDNA is derived from 3 overlapping CDNA clones, designated plasmid pRH4-23 (ATCC 67885), plasmid pRH4-23 (ATCC 67887). A virus/clrcular DNA plasmid vector comprising the cDNA may be transformed or transfected into a
                                 The sequence is derived from 3 overlapping clones, pRH3-1,pRH4-23, and pRH14-31. (Deposited as ATCC 67885, 67886, and 67887 resp.) The clones were isolated from a CDNa library in the lambda Zap vector prepd. from mRNA obtd. from newborn rat hearts using rat brain II cDNA probe. The isolated DNA can be used to screen a
                                                                                                 human derived cardiac cDNA library for the corresponding
ne. Proteins produced by expression of the DNA have
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sodium channel protein; ds; therapeutic; diagnostic; prognostic;
                                                                                                                                                                                                                  0;
                                                                                                                                                                                        Score 18.2; DB 11; Length 7555; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Purified DNA's encoding rat and human cardiac sodium channel protein - useful for recombinant expression to produce sodium
                                                                                                                                                  Sequence 7555 BP; 1576 A; 2314 C; 2101 G; 1564 T; 0 other;
                                                                                                                                                                                                                  3; Indels
                                                                                                                          diagnostic therapeutic, and prognostic applications.
                                                                                                                                                                                                                                                                                                                                                                                                            Cardiac sodium channel protein coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                          1 tcagccagttccaccccgtgcac 23
          Claim 7; Fig 1; 65pp; English.
                                                                                                                                                                                         Query Match
Best Local Similarity 87.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JAN-1995
                                                                                                                human gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rogart RB;
                                                                                                                                                                                                                                                                                                                                                         AAQ81328;
                                                                                                  similar
                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amplification using primers corresponding to highly conserved sequences of non-structural proteins NS5 and NS4. Products were cloned into pUC18 and expressed in Escherichia coli. NS5 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotide(s) specific for hepatitis C virus types 4, 5 and 6 - and related antigenic peptide(s) and antibodies, useful in vaccines, diagnosis, HCV typing and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HCV-4; HCV-5; HCV-6; NS4; NS5; non-structural protein; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody; vaccine; diagnosis; therapy; typing; immunoassay; ss.
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0
                                                                                                           75.8%; Score 18.2; DB 16; Length 7555; 87.0%; Pred. No. 1.2e+02; tive 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 73.3%; Score 17.6; DB 15; Length 57; Best Local Similarity 83.3%; Pred. No. 1.6e+02; Matches 20; Conservative 0; Mismatches 4; Indels (
Sequence 7555 BP; 1577 A; 2309 C; 2103 G; 1566 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viral RNA from HCV-infected patients was subjected to PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 57 BP; 14 A; 16 C; 13 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus type-specific sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 57; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 tcagccagttccaccccgtgcacg 24
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                                                                                                                                                                                                                                                                                                                                                 539 tcagccccttccaccccgtgcgc 561
                                                                                                                                                                                                                                                                      1 tcagccagttccacccgtgcac 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (COMM-) COMMON SERVICES AGENCY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ73770 standard; cDNA; 57 BP
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17-MAY-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Untranslated region; UTR; RNA binding protein; RBP; neurodegeneration; stroke; cardiovascular disease; hypertension; cancer; inflammation; metabolic disorder; obesity; diabetes; beta-2 adrenergic receptor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human beta-2 adrenergic receptor UTR region with RBP binding ability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072).

The sequence data for this patent did not form part of the printed
                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Pred. No. 2.7e+02;
0; Mismatches 1; Indels 0;
                                                                Drosophila melanogaster genomic polynucleotide SEQ ID NO 23689.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 23689; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4541 BP; 1232 A; 1097 C; 1013 G; 1199 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                        Myers EW
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11-JUL-2000; 2000US-0614150
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                                26-MAR-2002 (first entry)
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nes 18; Conservative
                                                                                                               pharmaceutical; gene; ds
                                                                                                                                             Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                        Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                         (PEKE ) PE CORP NY.
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                                                                                                                                                                            WO200171042-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        interactions
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   ABL24072;
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Sequences AAH27131 - AAH27151 represent human gene untranslated regions where the corresponding mRNA fragment has RNA binding protein (RBP) binding activity. RBPs mediate the processing of pre-mRNA, the transport of mRNA from the nucleus to the cytoplasm, mRNA stabilisation.

Translational efficiency, and the sequestration of some mRNAs. Therefore modification of post-transcriptional protein expression in eukaryotic cells may be carried out through the targeting specific interactions of proteins that bind to RBPs. The gene fragments of the invention are used to identify their optimized sub-fragments, compounds that affect RNA/RBP interaction or mRNA functionality; or RBPs that interact with the compounds identified using the gene fragments are potentially useful for therapeutic regulation of gene expression, such as in cases of neurodegeneration; stroke; cardiovascular disease; hypertension; cancer; inflammation; metabolic disorders (Obesity and diabetes) and bacterial or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                viral infection. The present sequence is one of gene fragments of the
                                                                                                                                                                                                                                                                                                                                 New nucleic acids that bind RNA-binding proteins or regulate mRNA function, useful for therapeutic gene regulation, such as in cases of neurodegeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention, isolated from the human beta-2 adrenergic receptor gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Component; rat; proteosome; vector; transformant; tumours; diagnosis; expression vector; ss.
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/product= rat_proteosome_RING12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ54681 standard; cDNA to mRNA; 657 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 28; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 caqccaqttccacccqtqcac 23
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                                                                   99US-0437458.
09-NOV-2000; 2000WO-US30888
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                                                                                                                                          (MESS-) MESSAGE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19; Conservative
                                                                                                                                                                                                                 Giordano A, Xavier AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 657
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                                                                                                                                                                                                                                                                                    WPI; 2001-335904/35
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                                                                       10-NOV-1999;
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                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                        Sequences (AAQS4678-81) show various components of a rat proteosome. The component is useful for the elucidation of various mechanisms of diseases such as malignant tumours and their diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; single nucleotide polymorphism; SNP; MPL; chromosome 1p34;
                                                                                             A component of rat proteosome - for elucidation of mechanism of
                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                        Query Match 71.7%; Score 17.2; DB 15; Length 657; Best Local Slmilarity 86.4%; Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                    Sequence 657 BP; 137 A; 184 C; 198 G; 138 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reference sequence for human MPL gene exons 9-10.
                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                  (BIOM-) BIO MATERIAL KENKYUSHO KK.
                                                                                                                                 Claim 8; Page 5-6; 24pp; Japanese.
                                                                                                                                                                                                                                                                                                                     275 TCCTCCAGTTCCAACCCGTGCA 254
                                                                                                                                                                                                                                                                                                                                                                                          AAS19511 standard; DNA; 1785 BP
                                                                                                                                                                                                                                                                                                        1 tcagccagttccaccccgtgca 22
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            92JP-0154184.
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1028..1124
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                                                                                                                                                                                                                                                                                 19; Conservative
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                                                                                                          e.g. malignant tumour
                                                          WPI; 1994-011024/02.
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                                                                        P-PSDB; AAR47473
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          22-MAY-1992;
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oncogene (MPL) gene, useful for studying the function of and expressing \overline{\rm MPL} protein for use in screening drugs for treating diseases related to
                                                                                                        The present invention relates to novel single nucleotide polymorphisms (SNPs) in the human myeloproliferative leukaemia virus oncogene (MPL) gene located on chromosome lp34, and methods for haplotyping and/or allele-specific objects the methods of the invention make use of primer-extension oligonucleotides (ASOs) as probes and primers and/or The polymucleotides for detecting MPL gene polymorphisms. The polymucleotides and screened compounds are useful for the treatment of diseases associated with MPL activity, such as companital amegakaryocytic thrombocytopaenia (CAMT). The present sequence represents a reference sequence for human MPL gene exons 9-10. Note: This sequence encodes for only part of the MPL protein shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                    71.7%; Score 17.2; DB 24; Length 1785; 86.4%; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                           Sequence 1785 BP; 317 A; 562 C; 500 G; 403 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding novel human diagnostic protein #27614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 27614; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1672 tcagcctgttctaccctgtgca 1693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS91810 standard; cDNA; 1972 BP
                                                                           Claim 27; Fig 3; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 tcagccagttccaccccgtgca 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-2000; 2000US-0540217. 23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 86.48 Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; ABG27623.
                                         MPL activity -
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                                                                                                                                                                                                                                                                                                                           in AAU09495.
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polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (1) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in disorders forensists, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amno acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Sectification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glucoamylase P; hormoconis resinae; debranching activity; enzyme; dextrinase activity; Trichoderma reesei; starch granule; preservation; hydrolysis; gelatinised starch; glucose syrup; straight linear dextrin; saccharification; lignocellulosic material; sugar utilisation;
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hormoconis resinae glucoamylase P gene construct - for transforming
                                                                                                                                                                                                                                                                                                                                                                                   ;
0
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Pred. No. 3.1e+02;
0; Mismatches 3; Indels 0;
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                                                                                                                                                                                                                                                                                                    Sequence 1972 BP; 460 A; 523 C; 552 G; 437 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Korhola M,
                                                                                                                                                                                                                                                      specification, but was obtained in electroni
at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Joutsjoki V,
Vainio A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT90830 standard; cDNA; 1996 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                     cagccagttccacccgtgcac 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA encoding glucoamylase P.
                                                                                                                                                                                                                                                                                                                                                      71.78;
86.48;
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9505-0385370.
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2515..2520
/*tag= b
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                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 86.4*
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Torkkeli H, Torkkeli T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ALKO-) ALKO-YHTIOT OY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-456802/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hormoconis resinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        feed additive; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAW30155
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AATYONS UP and AATYONS I represent the close and accounty the composition of the invention and are capable of being processed by a Trichoderma host cell. H. resinae glucomylase P has higher a Trichoderma host cell. H. resinae glucomylase P has higher debranching and dextrinase activity than conventional glucomylase-pullulanase mixtures. T. reesei secretes enzymes that are important for the degradation of complexes around and in starch granules. The recombinant glucomylase P enzyme produced by the Trichoderma host cell is useful in applications requiring the hydrolysis of gelatinised starch or the presence of a debranching activity. These applications in clude starch analysis, the manufacture of glucose syrups, production of straight linear dextrin for use in food, medicines and cosmetics, and in the preparation of food fibers by the enzyme to laundry and dish washing detergents, in wood and textile industry applications such as the preparation of plywood adhesives. It can also be used in the sacrification of lignocellulosic materials, the preservation of protein-containing animal or vegetable fodder, the preparation of products and to improve utilisation of sugar present in such feedstuff. When used as a feed additive for food animals, the recombinant bacterial blommass may be added directly to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                beta2 adrenergic receptor; genetic variation identification; hypertrophy; disease diagnosis; hypertension; prostatic disease; pulmonary disorder; asthma; peripheral vascular disorder; neuropsychic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pairs of oligonucleotides for amplifying adrenergic receptor genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 17.2; DB 18; Length 1996; Pred. No. 3.1e+02; 0; Mismatches 3; Indels 0;
                                                                          AAT90830 and AAT90831 represent the cDNA and gene encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AlphalB-adrenergic receptor; human; cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1996 BP; 474 A; 574 C; 491 G; 457 T; 0 other;
Trichoderma to produce recombinant glucoamylase P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human beta2-adrenergic receptor gene.
                                     Claim 2; Column 55-58; 61pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1473 tccgccagctccaccccgggca 1494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.7%;
86.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REGC ) UNIV CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9924454-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAY-1999
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Thy plans and the state of the 
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                                                                                is amplified by the primers of the invention. The primers are non-self hybridising; contain at least 15 nucleotides (nt) and has a melting
                                                        This sequence represents the human beta2-adrenergic receptor gene, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polymorphism; polymorphic marker; cardiovascular disease; myocardial infarction; unstable angina; hypertension; atherosclerosis; stroke; prognosis; drug screening; treatment outcome; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assessing cardiovascular status in humans involves comparing test polymorphic pattern comprising polymorphic positions within genes encoding specific proteins, with reference polymorphic pattern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.7%: Score 17.2; DB 20; Length 2300; 86.4%; Pred. No. 3.1e+02; tive 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2300 BP; 495 A; 613 C; 646 G; 546 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andersson MK, Lindstrom PHR, Jonsson L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human beta-adrenergic receptor-2 coding region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beta-adrenergic receptor-2 gene; coding region;
Disclosure; Fig 2; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        large-scale sequencing analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA38340 standard; DNA; 2305 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 cagccagttccacccgtgcac 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0104302.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of genetic alterations not
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Best Local Similarity 86,49
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Disclosure; Page 124-125; 126pp; English.

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cardiovascular disorders such as mycocardial infarction, unstable angina, hypertension, atherosclerosis and stroke. They are also useful for predicting the likely cardiovascular status of a patient given a retained the likely cardiovascular status of a patient given a retained regimen comprising administration of cardiovascular drugs (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-blockers) one or more polymorphic markers browides a basis for predicting the outcome of a treatment regimen. Fragments of the genes comprising a polymorphic site may be used as primers and probes for detecting genetic polymorphisms or in molecular trays for high throughput screening. The genes, and the proteins they encode are useful in the screening of potential cardiovascular drugs. Determination of an individual's polymorphic pattern reduces or infaintante patients from chinical trials who are predicted to be non-responsive, or at a risk for an adverse response, to a particular treatment regimen. Adverse results in an early trial can be evaluated to identify polymorphic patterns so that the adverse results can be evaluated correlated with a sub-population of the test population, permitting exclusion of such sub-populations from the treatment group. Beneficial drugs can be approved for use in the appropriate population, thereby in the case of the number of patients required for a patient which in
The invention relates to a novel method of assessing the cardiovascular status in an individual and to newly identified polymorphisms in the status in an individual and to newly identified polymorphisms in the receptor type 1 (ATI) and type 2 (ATI), angiotensinogen (ACT), renin, aldosterone synthase, endothelin receptor type A and beta-adrenergic receptors 1 and 2. The method comprises determining the sequence at one or more polymorphic positions within these genes, and comparing the pattern of polymorphisms from the individual with a reference polymorphic predetermined cardiovascular disease status. The polymorphic markers are useful for determining the predisposition of an individual to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         decreasing the number of patients required for a clinical trial, which in turn decreases the duration and cost of such trials. The present sequence represents the human beta-adrenergic receptor-2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coding region (GenBank Y00106/g293708). The polymorphic sites identified are 839A/G, 872C/G, 1045A/G, 1284C/T, 1316A/C, 1846C/G, 2032A/G, 2068 no insert/G/C and 2070 no insert/C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; adrenergic receptor; beta2 adrenergic receptor; beta2AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.7%; Score 17.2; DB 21; Length 2305; 86.4%; Pred. No. 3.1e+02; Live 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2305 BP; 495 A; 616 C; 649 G; 545 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "beta2 adrenergic receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human beta2 adrenergic receptor beta2AR gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          616 CTGCCAGTTCCAGCCCGTGCTC 595
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Hormoconis resinae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a fragment of the C allele of the human beta2 adrenergic receptor (beta2AR) gene, which is located on chromosome the presence of two copies of the T alleles, and it has been shown that the presence of two copies of the T allele leads to higher expression of the gene. This is because the polymorphism is found in the 5' leader beta2AR gene. The polymorphism is thought to affect individuals' responses to beta-agonists and beta-antagonists, and is likely to influence their predisposition to asthma, hypertension, congestive heart failure, ischemic heart disease, arrhythmia, obesity, diabetes, vascular disease, premature labour, migraine, anaphylaxis and chronic obstructive pulmonary disease (COPD). The gene can, therefore, be used to predict the susceptibility of an individual to these diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glucoamylase P; hormoconis resinae; debranching activity; enzyme; dextrinase activity; Trichoderma reesei; starch granule; preservation; hydrolysis; gatatinised starch; glucose syrup; straight linear dextrin; saccharification; lignocellulosic material; sugar utilisation; feed additive; ss.
                                                                                                                                                                                                                                                                                                                                                          Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic receptor (beta 2 AR), useful for predicting genetic disposition to a disease modified by beta 2 AR expression e.g. congestive heart failure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
'note= "no stop codon given at 3' end of sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2340 BP; 498 A; 627 C; 653 G; 562 T; 0 other;
                          1487..1546
/*tag= b
/label= 5'_leader_cistron
replace(1541,T)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Figure 1; 56pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     determine the best treatment.
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1588..2340
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Matches 19; Conservative
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            'partial
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                            sig_peptide
                                                                                                      mat_peptide
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                                                                                                                                                                                                                                                                                                     Liggett SB;
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Hormoconis resinae glucoamylase P, respectively. These sequences are used in the composition of the invention and are capable of being processed by a Trichoderma host cell. H. resinae glucoamylase P has higher debranching and dextrinase activity than conventional glucoamylase-pullulanase mixtures. T. reesel secretes enzymes that are important for the degradation of complexes around and in starch granules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hormoconis resinae glucoamylase P gene construct - for transforming Trichoderma to produce recombinant glucoamylase P \,
                                                                                                                                                                                                                                             /number= 1
/note= "designated IVS (intervening sequence) 1"
594..898
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1637..2447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT90830 and AAT90831 represent the cDNA and gene encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "encodes residues 178 to 347"
1584..1636
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2448..2745
                                                                                                                                                                                                                                                                                                                          /number= 2
/note= "encodes residues 76 to 177"
                                                                                                                                                                      /number= 1
/note= "encodes residues 1 to 75"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Column 60-66; 61pp; English.
Location/Qualifiers
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2515..2520
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                                       /*tag=
87..90
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P-PSDB; AAW30155.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-AUG-1993;
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07-FEB-1995;
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                                                                                                TATA_signal
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starch or the presence of a debranching activity. These applications starch or the presence of a debranching activity. These applications starch or the presence of a debranching activity. These applications include starch manalysis, the manufacture of glucose syrups, production of straight linear dextrin for use in food, medicines and cosmetics, and in the preparation of food fibers by the enzymatic treatment of seed husks or brans. The enzyme can also be used as an additive to laundry and dish washing detergents, in wood and textile industry applications such as the preparation of plywood adheaves. It can also be used in the saccharification of lignocellulosic materials, the preservation of feedstuff from meat by products and to improve utilisation of sugar present in such feedstuff. When used as a feed additive for food animals, the recombinant bacterial biomass may be added directly to the
The recombinant glucoamylase P enzyme produced by the Trichoderma host
                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reactions upon regular administration - by identifying patients homozygous for allele encoding Arg at position 16 of
                                                                                                                                                                                                                                                                                                                                              71.7%; Score 17.2; DB 18; Length 2745; 86.4%; Pred. No. 3.1e+02; tive 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diagnosing asthma patients predisposed to adverse beta-agonist
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/note= "A to G substitution, results in Arg16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beta-2-adrenergic receptor; human; asthma; beta-agonist;
                                                                                                                                                                                                                                                                                         Sequence 2745 BP; 643 A; 760 C; 667 G; 675 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human beta-2-adrenergic receptor cDNA.
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Best Local Similarity
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neuroprotector; immunosuppressor; predisposition; high blood pressure; cardiovascular disease; myocardial infarction; anxiety; depression; neuropsychiatric disease; attention deficit disorder; hyperactivity; eating disorder; anorexia nervosa; bullimia; migraine; allergy; drug; post-traumatic stress disorder; autonomous nervous system disease; metabolic illness; gene therapy; pharmaceutical intervention therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid sequence represented in AAZ00773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid sequence represented in AAZ00773"
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                                            AAW7577) having an arginine residue at position 16. A novel method for identifying individuals susceptible to adverse responses to regular administration of beta agonists comprises: (a) identifying in a genomic nucleic acid sample from the individual first and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                             second alleles of the beta 2-adrenergic receptor gene, and (b) classifying an individual as susceptible if first and second alleles both encode Arg at residue 16 of the beta 2-adrenergic receptor protein. Beta 2-adrenergic receptor protein. Beta 2-adrenergic receptor protein. Beta 2-adrenergic receptor protein. Beta 2-adrenergic receptor gene alleles may be identified by any known method e.g. denaturing gel electrophoresis or PCR amplification (see also AMYS5615-17). Identification preferably comprises amplifying a portion of each allele which includes the sequence encoding residue 16, and optionally also comprises determining nucleotide sequences of these portions (e.g. by automated sequence analysis). The invention identifies a known polymorphism in the beta 2-adrenergic receptor gene as being linked
                   This cDNA sequence codes for human beta-2-adrenergic receptor (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "This nucleotide differs from the wild type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
                                                                                                                                                                                                                                                                                                                                                                                               to adverse responses to regular beta-agonist administration; position 16 of the encoded protein can be either Arg or Gly, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 17.2; DB 19; Length 3451;
Pred. No. 3.2e+02;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                individuals homozygous for Arg16 are more susceptible.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human beta 2-adrenergic receptor DNA variant 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ00774 standard; DNA; 3451 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      replace(1120,g)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 cagecagttccaccccgtgcac 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            replace(159,t)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       replace(245,a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             replace(565,g)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.78;
86.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tag=
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Best Local Similarity
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Claim 2; Fig 2a; 27pp; German.

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/*tag= o
/note= "This nuclectide differs from the wild type
nucleic acid sequence represented in AAZ00773"
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nucleic acid sequence represented in AAZ00773"
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nucleic acid sequence represented in AAZ00773"
                                                                 /note= "This nucleotide differs from the wild type
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replace(1541,t)
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/note= "This nucleotide differs from the wild type
nucleic acid sequence represented in AZ00773
and results in a change in the corresponding
wild type amino acid sequence from an Ile
residue to Thr residue"
                          nucleic acid sequence represented in AA200773"
                                                                                                                     /_cds_ "his nucleotide differs from the wild type nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding wild type amino acid sequence from an Cys residue to Arg residue"
                                                                                                                                                                                                                                                                                /note= "This nucleotide differs from the wild type
nucleic acid sequence represented in AAZ00773
and results in a change in the corresponding
                                                                                                                                                                                                                                                                                                                                                                                    This nucleotide differs from the wild type nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding
/*tag= e
/note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                          wild type amino acid sequence from an GIY residue to Arg residue"
                                                                                                                                                                                                                                                                                                                                                                                                                             wild type amino acid sequence from an Glu
residue to Gln residue"
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                                         replace(1221,c)
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This invention describes novel variant human beta 2-adrenergic receptor gene sequences which have hypotensive, cardiant, neuroprotective and immunosuppressive activity. The products of the invention are used in a method to determine a predisposition for high blood pressure as well as method to determine a predisposition for high blood pressure as well as for abnormal blood pressure and other cardiovascular diseases, including myocardial infarction and stroke. Other conditions that can be determined include neuropsychiatric disease, such as depression, anxiety, attention deficit disorder with hyperactivity, eating disorder. Diseases of the autonomous nervous system, e.g. Bradbury-Egglesston, SNy-Drager and Riley-Day syndromes having selective noradrenergic-receptor disposition, or migraine, allergic conditions, e.g. asthma and atopic disorders, and metabolic illnesses, e.g. morbid obesity including predicting a change in weight, using body mass index, can also be determined. The beta 2-adrenergic receptor sequence variants can be used to develop therapeutics and/or lifestyle drugs. Individual specific beta 2-radrenergic receptor appoint sequence represents a variant of the wild type human beta 2-adrenergic receptor gene which is represented in AA200773.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Pred. No. 3.2e+02;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3451 BP; 794 A; 871 C; 892 G; 894 T; 0 other;
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Job time: 17382 sec
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86.4%;
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Best Local Similarity 86.4
Matches 19; Conservative
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ORGANISM
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                                                                                                                                                                                                                                                                                                                     RESULT
AX349069
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KEYWORDS
SOURCE
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                                                  (without alignments)
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                                          July 31, 2002, 14:01:55; Search time 6034.22 Seconds
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       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                 1797656 seqs, 10463268293 residues
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Maximum Match 100%
Listing first 45 summaries
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Description

Score Match Length DB

Query

Result No.

SUMMARIES

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AP003792 Oryza sat
AL663090 Oryza sat
AC078802 Homo sapi
AC068854 Homo sapi
AC011585 Homo sapi
AC011585 Homo sapi
AC07849 Homo sapi
AC158608 Mus muscu
AF391350 Stiphodon
U33423 Molluscum c
U52849 Molluscum c
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AJ32832 Homo sapi
AC06275 Giardia i
AC074924 Giardia i
AJ303372 Rattus no
AX34083 Sequence
AR353637 Rattus no
AR35962 Rat cardiac
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                                              Ac028268 Giardia i
Ac080286 Giardia i
Ac072500 Giardia i
Ac070455 Giardia i
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AR128599 Sequence
AJ428570 Thauera a
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AC091510 Leishmani
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AC099583 Mus muscu
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AX349063 Sequence
AC103298 Rattus no
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/db_xref="taxon:32630"
/note="Oligonucleotide"
11 c 5 g 4 t
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Sequence 7 from Patent W00202785.
AX349069
AX349069.1 GI:18615104
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AC101702
AC099583
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AP003792
AC053N00210
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AR128599
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                       86.0 177696
78.3 959
78.3 950
78.3 32490
76.7 113288
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC103298 177696 bp DNA linear HTG 21-DEC-2
Rattus norvegicus clone CH230-75J23, *** SEQUENCING IN PROGRESS
***, 66 unordered pieces.
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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100.0%; Score 24; DB 6; Length 24; 100.0%; Pred. No. 5.1; tive 0; Mismatches 0; Indels
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Sequence 1 from Patent WO0202785.
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Hellins, B., Homsi, F., Howard, S., Huber, J., Hulk, S., Hume, J., Hullins, B., Homsi, F., Howard, S., Huber, J., Hulk, S., Hume, J., Jackson, L. B., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Juckson, L. B., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Juckson, C., Karlson, J., Karlson, J., Karlson, J., Karlson, J., Karlson, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulsegd, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Martinez, E., Massey, E., Mawhiney, E., Martinez, E., Morsie, M., Morris, S., Moser, M., Newtson, J., Newtson, J., Neysen, A., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuon, G., Oraqunye, N., Orado, R., Parker, M., Petez, L., Peters, L., Pickens, R., Primus, E., Pu, L., Oulles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Shoshtari, N., Sisson, I., Sodergren, E., Soneike, T., Sparks, A., Stanley, H., Tamerisa, R., Tang, H., Tang, H., Taylor, C., Taylor, T., Tellarod, B., Tomes, N., Thomas, S., Walliams, G., Warren, R., Washington, C., Walliams, G., Walliamson, A., Walezyk, R., Rooden, S., Warlington, S., Walliams, G., Walli
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NOTE: This is a 'working draft' sequence. It currently consists of 66 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C.,
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Consensus quality: 151283 bases at least 030
Consensus quality: 159356 bases at least 020
Estimated insert size: 148940; sum-of-contigs estimation
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On Dec 21, 2001 this sequence version replaced gi:17062960.
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contig of 7012 bp in length
spap of unknown length
contig of 5493 bp in length
gap of unknown length
contig of 4974 bp in length
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gap of unknown length
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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Worley, K.C.
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gap of unknown length
contig of 1909 bp in length
gap of unknown length
contig of 3217 bp in length
gap of unknown length
gap of unknown length
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bp in length
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                                                                                                unknown length
of 3092 bp in length
                                                                                                                unknown length
of 3240 bp in length
                                                                                                                                                                                                                                                                                                                                    of 2285 bp in length
unknown length
of 2024 bp in length
                                                         bp in length
                                                                        bp in length
                                                                                         bp in length
                                                                                                                                                                                                       of 1937 bp in length
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bp in length
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of 1383 bp in length
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of 3640 bp
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unknown le
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of 4587 b
unknown 1
of 4269 b
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of 4861 h
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of 4599 h
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of 2885 l
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of 2720 h
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of 2282
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of 1911
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of 1849
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of 2192
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gap of unknown
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Giardia intestinalis clone CI0266 ștrain WB-C6, LOW-PASS SEQUENCE SAMPLING.
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Hinkle G., Holder M.E., Sogin M.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Giardia intestinalis
Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia
                            in length
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bp in length
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bp in length
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of 1378 bp in length
unknown length
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* sequencing reads that have not been assembled into
                                                                                               Length
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05-APR-2000 (Rel. 63, Last updated, Version 1)
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  gap of unknown I contig of 2046 by a per of unknown I contig of 1173 by app of unknown I contig of 1276 by app of unknown I contig of 1276 by app of unknown I contig of 2012 by app of unknown I contig of 1090 by app of unknown I contig of 1903 by app of unknown I contig of unknown I
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of 1525
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of 1490 l
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of 1378
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AC028268/c
ID AC028268 standard; DNA; HTG; 959 BP.
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87.5%;
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Best Local Similarity 87.59
142743
142843
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Location/Qualifiers
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nes 20; Conserva
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                              * be preserved.
                                                                                                                                                                         Sequence 960
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                                                                                               source
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                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Giardia intestinalis clone AJ2336 strain WB-C6, LOW-PASS SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (28-SEP-2000) to the EMBL/GenBank/DDBJ databases.
Josephine Bay Paul Center for Comparative Molecular Biology and Evolution,
Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McArthur A.G., Morrison H.G., Nixon J., Eakin N.Q., Kim U., Crocker M.C., Hinkle G., Holder M.E., Sogin M.L.;
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                            78.3%; Score 18.8; DB 33; Length 959; 90.9%; Pred. No. 6.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
                                                                                                                                                                                                                                                                                                                       2; Indels
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sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
voverlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
arbitrary. LOW-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                      Sequence 959 BP; 226 A; 251 C; 259 G; 216 T; 7 other;
                                                                                  * will be sequenced to completion. In the event that
                                                                    · However, it should not be assumed that this clone
                                                                                               * the record is updated, the accession number will
                                                                                                                                                                                                     /organism="Giardia intestinalis"
                                                                                                                        959: contig of 959 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-SEP-2000 (Rel. 65, Created)
29-SEP-2000 (Rel. 65, Last updated, Version 1)
                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; DNA; HTG; 960 BP.
                                                                                                                                                                                       /db_xref="taxon:5741"
                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                              /clone="CI0266"
                                                                                                                                                                                                                                                                                                                                                                           265 AGCCAGGTCGACCCCGTGCACG 244
                                                                                                                                                                                                                  /strain="WB-C6"
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                                                                                                                                                                                                                                                                                                                       20; Conservative
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                                                                                                                                                                                                                                                                                                           Best Local Similarity
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                                                                                                              be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished.
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                                                                                                                                                                                                                                                                                                                         Matches
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Giardia intestinalis clone NJ4295 strain WB-C6, LOW-PASS SEQUENCE SAMPLING.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18.8; DB 33; Length 960;
Pred. No. 6.7e+02;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (07-JUN-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 219 A; 256 C; 248 G; 237 T; 0 other;
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* will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         However, it should not be assumed that this clone
                               * the record is updated, the accession number will
                                                                                                                                                                                                                                                                                        /organism="Giardia intestinalis"
/strain="WB-C6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           972: contig of 972 bp in length.
                                                                                              960: contig of 960 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-JUN-2000 (Rel. 64, Created)
13-JUN-2000 (Rel. 64, Last updated, Version 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This record contains 1 individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; DNA; HTG; 972 BP
                                                                                                                                                                                                                                                                       /db_xref="taxon:5741"
                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         /clone="AJ2336"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   843 AGCCAGATCGACCCCGTGCACG 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 agccagttccacccgtgcacg 24
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90.9%;
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DEFINITION
                                                                                                                                                                                                                                                                                                   ORGANISM
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AUTHORS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                    SME591790
                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUBMED
                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                           VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                      SOURCE
       XX
So XX
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                                                                                                                                                                                                                                                                                                                                                                                                                      Giardia intestinalis clone EJ6686 strain WB-C6, LOW-PASS SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (06-JUN-2000) to the EMBL/GenBank/DDBJ databases.
Josephine Bay Paul Center for Comparative Molecular Biology and Evolution,
Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA
                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Morrison H.G., McArthur A.G., Nixon J., Eakin N.Q., Kim U., Crocker M.C., Hinkle G., Holder M.E., Sogin M.L.; "Giardia: a model for ancient eukaryotic genome analysis"; Unpublished.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eakin N.Q., Morrison H.G., McArthur A.G., Nixon J., Kim U., Crocker M.C.,
Hinkle G., Holder M.E., Sogin M.L.;
                                                                                                                                                                        Gaps
                                                                                                                                                                        ;
0
                                                                                                                                        Score 18.8; DB 33; Length 972;
Pred. No. 6.7e+02;
); Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allow overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                              Sequence 972 BP; 221 A; 250 C; 268 G; 231 T; 2 other;
                          /db_xref="taxon:5741"
/organism="Giardia intestinalis"
/strain="WB-C6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Giardia intestinalis"
/strain="WB-C6"
/clone="EJ6686"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      990: contig of 990 bp in length.
                                                                                                                                                                                                                                                                                                                                                                            13-JUN-2000 (Rel. 64, Created)
13-JUN-2000 (Rel. 64, Last updated, Version 1)
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                                                                                                                                                                                                                                                                                              standard; DNA; HTG; 990 BP.
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                                                                     /clone="NJ4295"
                                                                                                                                                                                                           460 AGCCAGATCGACCCCGTGCACG 481
                                                                                                                                                                      ő
                                                                                                                                                                                              3 agccagttccaccccgtgcacg 24
                                                                                                                                      Query Match 78.3%;
Best Local Similarity 90.9%;
Matches 20; Conservative
              1. .972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Giardia intestinalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG; HTGS_PHASE0
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ID AC070455
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FT FT XX XX SO SO SO
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EU Consortium
MELILO EU Consortium
Laboratoire de Biologie Moleculaire des Relations
Plantes-Microorganismes, UMR215-CNRS-INRA, BP27, F-31326 Castanet,
France, Laboratoire de Genetique et Developpement UMR6061-CNRS,
France, CATC Gmbh, Fritz-Annold-str. 23, D-78467 Konstanz, Germany,
Universitaet Bielefeld, Biologie IV (Genetik) Universitaetstr 25,
D-33615 Bielefeld, Germany, Unite de Biochimie physiologique,
Universite Catholique de Louvain, Place Croix du Sud 2, Bte 20,
B-1348 Louvain-la-Neuve, Belgium, Unite de Microbiologie, Faculte
des Schences Agronomiques de Gembloux, Avenue Marechal Juin 6,
B-5030 Gembloux, Belgium. E-mail:Jerome.Gouzy@toulouse.inra.fr
                                                                                                                                                                                                                                                                                                                                                                       323450 bp DNA linear BCT 16-AUG-2001
Sinorhizobium meliloti 1021 complete chromosome; segment 9/12.
AL591790 AL591688
AL591790.1 GI:15075731
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Boistard,P., Becker,A., Boutry,M., Cadieu,E., Dreano,S., Gloux,S.,
Godrie,T., Goffeau,A., Kahn,D., Kiss,E., Lelaure,V., Masuy,D.,
Pohl,T., Portetelle,D., Puehler,A., Purnelle,B., Ramsperger,U.,
Renard,C., Thebault,P., Vandenbol,M., Weidner,S. and Galibert,F.
From the Cover: Analysis of the chromosome sequence of the legume
symbiont Sinorhizobium meilloti strain 1021
Proceedings of the National Academy of Sciences of the United
11481430
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Submitted (26-JUL-2001) Gouzy J., Submitted on behalf of the MELILO
EU Consortium
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/note="Product confidence : hypothetical
Gene name confidence : hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                         Gaps
                                                                                                                                                   ;
0
                                                                                            Length 990;
                                                                                                                                                      Indels
Sequence 990 BP; 228 A; 273 C; 282 G; 206 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Sinorhizobium meliloti"
                                                                                         Score 18.8; DB 33;
Pred. No. 6.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
/evidence=not_experimental
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/protein_id="Cac46787.1"
                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            predicted by Codon_usage
predicted by Homology
predicted by FrameD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhizobiaceae; Sinorhizobium.
1 (bases 1 to 323450)
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/gene="SMc01575"
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/gene="SMc01575"
                                                                                                                                                                                                                                               800 AGCCAGATCGACCCCGTGCACG 779
                                                                                                                                                                                                          3 agccagttccaccccgtgcacg 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sinorhizobium meliloti. Sinorhizobium meliloti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 323450)
                                                                                         78.3%;
90.9%;
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                                                                            Query Match
Best Local Similarity 90.99
Matches 20; Conservative
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Q

gene

CDS

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WNLKTPRGTVTARHVILATNAYGSILVTGVPKKEYRQBELTILEYFQFATNPLEDNVAAR
ILDERQGAWDTGLVMTSFRMDRQNRLIFGSIGRLDAIAAGTHRAFAARSVRKLFPYIG
BYPREHWWNDGRIGMTYNNLPANHVLAPNVSISGYNGRGIAPGTVFGRALARHVTGDT
SAIPLAETPVYPDPWTTLSAFYHAGAQAKHFIDKRF"
complement (3024, 3740)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MATERALPNLWHATAPAAPRTAPLAGDLTVEVAIVGGGFTGLSA
ALHLAETGIRTAVIEARMIGFGGSGRNVGLVNAGWWQPDDLIATLGAAAGNRLLDEL
GDGPSFVYDLVAKHGIECEAVRNGTLHMSVGAEGLKEIREREAQWKKRGAPVEVLSAE
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TYSSEVSGRYANLEVISHVTPASLPCHIRELKGEADFIVIDLAGAKNDLAALAGLSD
HVLIPVQGCAMDARGAVQILELIRHIGEKARYRINSSYVLRYNSIVTTRALQTIKAL
LASRQVSVLDTPIVERYAYREIFECGGTLQMMDPNRVSNLDKARENAYALAAEVQNLL
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                                                           PEGDILDY I PGEAEVHAMRDRRGRTVLVDPWGNIVATVVPNDGYGRGGRRREYGRDGY
PEPRDRGYGY SEPGEFTGAIPEYRDIAPAPVEREDLPNSLPSLSDREEAAYDPQYDDP
LAQPMPPAMTVTGKSRAEIAALQVFLDREGFSPGVIDGKMGSNVTKAIEAWQQATGET
                                                                                                                                                 LDPNNTEDILERLRFNGGLPITTYTITAADAAGPFVASIPEDYAHKAOLPHLSFTSVT
BEMGERKHNDEAVLRELNGVDFSIGGTTIKVVNPGPNKKKKKYNRIVARKAKOKTALY
DEAGKLIAAYPSTIGSSDTSGPSGTVHYDERIAFDGTYTNPK INFOGANDRILOLOG
GPNGPVGTVWIALSKPTYGIHGTPEPSKIGKTQSHGCVRLTNWDATELGKMVSTGVTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="miscellaneous; hypothetical/global homology"
/note="product confidence: hypothetical
Gene name confidence: hypothetical
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product-"CONSERVED HYPOTHETICAL PROTEIN"
/protein_id="CAC46789.1"
/db_xref="G1:15075233"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /EC_number="1.1.1.-"
/function="small molecule metabolism"
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/note="Product confidence : putative
Gene name confidence : hypothetical
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
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Gene name confidence : hypothetical
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
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                                                                                                                                                                                                                                                                                            1/07. .2996
/gene="SMC01576"
1707. .2006
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/trans1_table=11
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gene

CDS

gene

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DKNGQYGMSELMRHYVAGQLAHASEVTYFLAPYINSYKRFWAGTFAPTKAIWSKDNRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MSYSFEELKEDVAAGRIDTVLACQVDMQGRLMGKRFHAEYFVES
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CDMLDHDTHAEVPHSPRAILKKQVARLEAMGFKAYMASELEFFLFDGSYDDARLSGYR
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                                                                    AGIALEGMELVREYLPRAYEGGADIEARANNMSAAAMGAVAPOKGLGAIHSESHPVGA
IYNTHHGWTNAVVMPPVLRFNRSAIEEKIGRAAAXLGIAGGFEVDYVLRLREELGV
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COMplement (5091. . 6476)

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APSTEKSVAWSNYKLGNPLDDETTLGAMANKFAATVRNQVADAISKGARALIDPKL
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SLWTKDAERAARIGGRDLETGTVFMNRADYLDPALCWTGVKETGRGGSLSVLGFHNLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGYRLCGEGSKAIRIECRVGGSDLNPYLAFAALIAAGIAGIENKMELEAPFVGDAYQG
KEVREIPHTLREAGEALSGSKMLRAAFGEEVVDHYVHAAEWEQQEYDRRVTDWEVARG
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                                                     SASHVKKVIFHPKFLPGVTICDPELTVGMPKVITAGTGMDAFAHCLEAYSSPFYHPMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LDERVKLVLAGVARLNEMVDEVVPELAWQMGRPVRYGGEFKGFNERSNYVASIAADAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPLVVEESDRFERRIAREPHGVVFVIAPWNYPYMTAINTVAPALMAGNTVILKHASQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILVGERMVRAFIEAGVPADVFONLFLDHDTTAALIAAKSFDFINFTGSVEGGRSIERA
PMAITQQALDILEAGGLGRAIFADVDPNPNDRNLEAGVKAFRDGGHDGVVAFGGGSGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="cell processes; transport of small molecules;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(6674. .8038)
/gene="SMc01594"
complement(6674. .8038)
/gene="SMc01594"
/function="miscellaneous; hypothetical/global homology"
/note="Product confidence: hypothetical
Gene name confidence: hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 323450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence-not_experimental
/product=rcONSENVED HYPOTHETICAL PROTEIN"
/protein_id="CAC46792.1"
/db_xref="G1:15075236"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                        complement(5091. .6476)
/gene="SMC01588"
/EC.unuber="1.2.1."
/function="small molecule metabolism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acids, amines, peptides"
/note="Product confidence : putative
Gene name confidence : hypothetical
                                                                                                                                                                                                                                                                                                                                     /note="Product confidence : putative
Gene name confidence : hypothetical
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18.8; DB 1;
Pred. No. 3.8e+02;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         predicted by Codon_usage
predicted by Homology
predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            predicted by Codon_usage
predicted by Homology
predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(8131. .9678)
/gene="SMc01597"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(8131. .9678)
/gene="SMc01597"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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90.9%;
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Matches 20; Conserv
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Dipublished

Dipagon, S., Barna, N., Bastlen, V., Boquslavkiy, L., Boukhgalter, B., Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Boquslavkiy, L., Boukhgalter, B., Erown, A., Camarata, J., Campoplano, A., Chang, J., Chazaro, B., Cooke, P., Darrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, M., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre N., Hagos, B., Hadford, A., Raratas, A., Kalls, C., LaRocque, K., Liu, G., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., McCarthy, M., McEwan, P., McHall, C., LaRocque, K., Mathews, C., Macdonald, P., Major, J., Matthews, C., Macdonald, P., Major, J., Matquis, N., Mathews, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D., O'Love, J., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riby, R., Schauer, S., Schupback, R., Strauss, N., Subramanian, A., Santos, R., Schauer, S., Schupback, R., Strauss, N., Subramanian, A., Travis, N., Travis, Travis, N., Travis, N., Travis, Travis, N., Travis, Travis, N., Travis, N., Travis, Travis, N., Travis, N., Travis, Travis, Travis, N., Travis, Travis, Travis, Travis, N., Travis, Tr
ACLU1702 113288 bp DNA linear HTG 23-NOV-2001
MUS musculus clone RP23-247G20, LOW-PASS SEQUENCE SAMPLING.
ACL01702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 113288)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This record contains 144 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of 100 bp contig of 683 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    670: contig of 670 bp in length
                                                                                                                                                                                                                                                                                                                                                                                          Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-247G20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: L17246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone name: 247_G_20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2344 3009: cor
3010 3109: gap of
3110 3792: cor
                                                                                                                                          AC101702.1 GI:17060477
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                                                                                                                                                                            HTG; HTGS_PHASEO.
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                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                     house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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                                                                   DEFINITION
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JOURNAL
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                                                                                                            ACCESSION
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JOURNAL
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SOURCE
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                                                                                                                                              VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Giardia intestinalis clone LJ0406 strain WB-C6, LOW-PASS SEQUENCE SAMPLING.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Morrison H.G., McArthur A.G., Nixon J., Eakin N.Q., Kim U., Crocker M.C., Hinkle G., Holder M.E., Sogin M.L.; "Giardia: a model for ancient eukaryotic genome analysis"; Unpublished.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nixon J., Morrison H.G., McArthur A.G., Eakin N.Q., Kim U., Crocker M.C.,
Hinkle G., Holder M.E., Sogin M.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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86.4%; Pred. No. 1e+03;
Live 1; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (06-FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP; 224 A; 247 C; 243 G; 213 T; 5 other;
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/strain="WB-C6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-FEB-2001 (Rel. 66, Created)
07-FEB-2001 (Rel. 66, Last updated, Version 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This record contains 1 individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .932
/db_xref="taxon:5741"
                                                                                                                                                                                                                                                       standard; DNA; HTG; 932 BP
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   466 AGCCAGATCGACCCCKTGCACG 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 19; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTG; HTGS_PHASEO
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9383 9482-925. cont.19 of 720 bp in length 10193 10292: gap of 100 bp 10293 10966: contig of 710 bp in length 10293 10966: contig of 674 bp in length 1067 11762: contig of 696 bp in length 1163 11863: gap of 100 bp 11863 12554: contig of 692 bp in length 1255 12654: gap of 100 bp 12555 1354: contig of 692 bp in length 13355 13454: gap of 100 bp 13355 13454: gap of 100 bp 13355 13449: contig of 695 bp in length 13455 13449: contig of 695 bp in length
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4672 5366: contig of 695 bp in length
5367 5466: gap of 100 bp
5467 6158: contig of 692 bp in length
6159 6258: gap of 100 bp
6259 6962: contig of 704 bp in length
6363 7062: contig of 688 bp in length
7751 7850: gap of 100 bp
7751 7850: gap of 100 bp
7751 8552: contig of 688 bp in length
8853 8652: contig of 702 bp in length
8853 8652: gap of 100 bp
88653 9382: contig of 730 bp in length
of 100 bp
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of 100 bp
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ассияться 233684 bp DNA linear HTG 16-NOV-2001 Mus musculus clone RP23-189G16, WORKING DRAFT SEQUENCE, 25 unordered pieces.
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Pred. No. 6.3e+02;
); Mismatches 1; Indels 0;
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47682: contig of 690 bp in length
882: gap of 100 bp
48493: contig of 711 bp in length
593: gap of 100 bp
49276: contig of 683 bp in length
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ap of 100 bp
:: contig of 691 bp i
33358: gap of 100 bp
34077: contig of 719 bp
34177: gap of 100 bp
34887: contig of 710 bp
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contig of 710 bp
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38857: contig of 704 bp
57: gap of 100 bp
39666: contig of 709 bp
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51660: contig of 657 bp
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38053: cont
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50096: cont
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AUTHORS TITLE JOURNAL REFERENCE AUTHORS

REFERENCE

KEYWORDS

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70203 70302: gap of 100 bp 70303 102493: contig of 32191 bp in length 102494 102593: gap of 100 bp 102554 116554: contig of 14061 bp in length 11655 116754: gap of 100 bp 116755 129262: contig of 12508 bp in length
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150868: contig of 21506 bp in length
                          5093 6602: courty ...
6603 6702: app of 100 bp
6703 10246: contig of 3544 bp in length
6703 10346: app of 100 bp
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27548: contig of 4085 bp in length
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  of 100 bp
contig of 1510 bp in length
                                                                                                46: gap of 100 bp
12129: contig of 1783 bp in length
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16558: contig of 2004 bp in length
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/note="assembly_fragment"
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/note="assembly_fragment"
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/db_xref="taxon:10090"
/clone="RP23-189G16"
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker:html
                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 233684)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center clone name: 189_G_16

Center clone name: 189_G_16

Sequencing vector: Plasmid; n/a; 100% of reads
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 2251791 bases at least Q40

Consensus quality: 229156 bases at least Q30

Consensus quality: 230361 bases at least Q20

Insert size: 241000; agarose-fp

Insert size: 231284; sum-of-contigs

Quality coverage: 11.5 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2200: gap of 100 bp 13332: contig of 1132 bp in length 3432: gap of 100 bp 4992: contig of 1560 bp in length
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                                                                                                                                                  Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-189G16
     HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
                                                                                                                                                                                                                              (bases 1 to 233684)
                                  house mouse.
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2201
3333
3433
                                                                                                                                                                                                    Unpublished
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TITLE JOURNAL

COMMENT

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Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre, Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens genomic sequence surrounding NotI site, clone HSJ-DG20RS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75.8%; Score 18.2; DB 33; Length 667; 87.0%; Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18.2; DB 9; Length 727; Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                              * identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
                                                                                               * sequencing reads that have not been assembled into excortigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 667 BP; 159 A; 143 C; 183 G; 176 T; 6 other;
                                                                                                                                                                                                                                                                                                        667: contig of 667 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:5741"
/organism="Giardia intestinalis"
/strain="WB-C6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA
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                                                                              * NOTE: This record contains 1 individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             727 bp
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239 c 217 q
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87.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           . 667
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                                                                                                                                                                                                                                                                                       be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Morrison H.G., McArthur A.G., Nixon J., Eakin N.Q., Kim U., Crocker M.C., Hinkle G., Holder M.E., Sogin M.L.; "Glardia: a model for ancient eukaryotic genome analysis";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McArthur A.G., Morrison H.G., Nixon J., Eakin N.Q., Kim U., Crocker M.C.,
Hinkle G., Holder M.E., Sogin M.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.7%; Score 18.4; DB 2; Length 233684; 95.0%; Pred. No. 5.9e+02; tive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2402 others
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02-AUG-2000 (Rel. 64, Last updated, Version 1)
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27649. .31362
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16755. .129262
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                                                                                                                                                                                                                                                                                02594. .116654
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ORIGIN

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Giardia intestinalis clone AJ2681 strain WB-C6, LOW-PASS SEQUENCE SAMPLING.
                                                                                                                                                                                                Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia
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02-AUG-2000 (Rel. 64, Last updated, Version 1)
                                  standard; DNA; HTG; 1102 BP
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                                                                                                                                                                                      Giardia intestinalis
                                                                                                                                                                HTG; HTGS_PHASE0
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           RESULT
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                                                                                                                                                                                                            Giardia intestinalis clone NJ4136 strain WB-C6, LOW-PASS SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (21-APR-2000) to the EMBL/GenBank/DDBJ databases.
Josephine Bay Paul Center for Comparative Molecular Biology and Evolution,
Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                             Morrison H.G., McArthur A.G., Nixon J., Eakin N.Q., Kim U., Crocker M.C., Hinkle G., Holder M.E., Sogin M.L.; "Giardia: a model for ancient eukaryotic genome analysis"; Unpublished.
                                                                                                                                                                                                                                                                                                                                                                                                   Nixon J., Morrison H.G., McArthur A.G., Eakin N.Q., Kim U., Crocker M.C.,
Hinkle G., Holder M.E., Sogin M.L.;
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 1.2e+03;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                     Eukaryota; Diplomonadida; Hexamítidae; Giardinae; Giardia
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 233 A; 237 C; 221 G; 213 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the record is updated, the accession number will
 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Giardia intestinalis"
/strain="WB-C6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 904: contig of 904 bp in length.
                                                                                                                                                                          26-APR-2000 (Rel. 63, Created)
26-APR-2000 (Rel. 63, Last updated, Version 1)
 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This record contains 1 individual
                                                                                                       standard; DNA; HTG; 904 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:5741"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              539 TCAGCCAGTGCCCCGCGTGCAC 561
                                     674 CAGCCAGGTCCACGCGGTGCACG 696
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                      2 cagccagttccacccgtgcacg 24
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87.0%;
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 Conservative
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                     HTG; HTGS_PHASEO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be preserved.
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20;
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                                                                                                                            AC062755;
                                                                                                      AC062755
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 Matches
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Josephine Bay Paul Center for Comparative Molecular Biology and Evolution,
Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA
Morrison H.G., McArthur A.G., Nixon J., Eakin N.Q., Kim U., Crocker M.C., Hinkle G., Holder M.E., Sogin M.L.; "Giardia: a model for ancient eukaryotic genome analysis";
                                                                                                                                                                                                                   MCArthur A.G., Morrison H.G., Nixon J., Eakin N.Q., Kim U., Crocker M.C.,
Hinkle G., Holder M.E., Sogin M.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         * sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1102 BP; 294 A; 283 C; 258 G; 265 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1102: contig of 1102 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18.2; DB 33;
Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Giardia intestinalis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This record contains 1 individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .1102
/db_xref="taxon:5741"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  546 TCAGCCAGTGCCCCCGCGTGCAC 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 tcagccagttccaccccgtgcac 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="WB-C6"
/clone="AJ2681"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.8%;
87.0%;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preserved.
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

July 31, 2002, 12:23:47; Search time 165.21 Seconds (without alignments) 17.842 Million cell updates/sec Run on:

US-09-899-718A-6 12 1 caggagcctcga 12 Title: Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

383533 seqs, 122816752 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_NA:* Database :

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	Sequence 147, App		3, 8	7	Sequence 2, Appli	1,	Sequence 14, Appl	14	14,	34,	Sequence 34, Appl	13,	Sequence 1, Appli	ı,	1,	ì	4	7,	Sequence 1, Appli	10	σ	22,	22,	83,	Sequence 1, Appli	Sequence 21, Appl	21,
SUMMARIES	ΩI	US-09-247-155-147	US-09-199-637A-266	US-09-221-275-3	US-09-341-587-2	US-09-221-275-2	US-09-221-275-1	US-08-449-645A-14	US-08-702-367A-14	PCT-US95-04681-14	US-08-222-616-34	PCT-US95-04228-34	US-09-428-711A-13	US-08-254-358-1	US-08-475-391-1	US-08-709-609-1	PCT-US95-07178-1	м	US-09-341-587-7	US-09-199-637A-1	-836-504A-	-08	US-08-358-171-22	US-09-090-947-22	US-08-594-031-83	US-08-047-041A-1	US-08-795-006A-21	US-09-184-073-21
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de	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7
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Appl Appl Appl Appl	Appli Appli Appli Appli Appli	Appl Appli Appl Appli Appli	Appli Appl Appl Appl	Appli Appli
12, 14, 13,	ດັດັດັດ	13, 8, 19, 11,	13, 13, 6,	1,
Sequence Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence
US-08-892-880-12 US-08-047-041A-14 US-08-370-975B-13 US-07-661-610C-14	US-09-609-324A-9 US-08-920-440B-9 US-09-173-492-9 US-09-173-133-9	US-09-269-617-13 US-08-278-630A-8 US-09-372-422A-19 US-08-356-180-1	US-08-892-880-1 US-08-765-662-13 PCT-US95-08745-13 US-08-941-445A-6	US-08-808-982-1 US-09-306-902A-1
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492 528 534 624	642 642 642 642	1025 1329 1454 1560	2313 2419 2419 2542	3014
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0 0				•

ALIGNMENTS

RESULT	RESULT 1 IIS-09-247-155-147/C
; Seque	Sequence 147, Application US/09247155A
; Pater; GENE	Patent No. 6312922 GENERAL INFORMATION:
; APPI	
; APP	APPLICANT: Duclert, Aymeric
; APPI	APPLICANT: Bougueleret, Lydie
; TIT	LE OF INVENTION: Complementary DNAS
FIL	FERENCE: GENSET.021A
· · CUR	CURRENT APPLICATION NUMBER: US/US/24/,155A
EAR	
EAR	FILING DATE: 1998-02
; EAR	APPLICATION N
; EAR	FILING DATE: 1998-04
; EAR	
; EAR	FILING DATE: 1998-08
; EAR	APPLICATION N
; EAR	
, NUM	NUMBER OF SEQ ID NOS: 182
SOF	••
; SEO	SEQ ID NO 147
E .	LENGTH: 475
; TY	
, OR	ORGANISM: Homo sapiens
; FE	FEATURE:
. NA	
٩	LOCATION: 146457
; FE	
. NA	NAME/KEY: sig_peptide .
S 	ION: 146292
;	INFORMATION:
. OT	INFORMATION: score 5.19999980
; OT	OTHER INFORMATION: seq CFLCLYPIPLCTS/HP
. EE	
, NA	NAME/KEY: polyA_signal
음 	
; FE	
, NA	
200	; LOCATION: 465475
US-07-	

Gaps ; 0 Query Match
100.0%; Score 12; DB 4; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels

; 0

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2001
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LENGTH: 2671
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US-09-221-275-1
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                                                                                                                                                                                                                  APPLICANT: Manuelle S. Shalina
APPLICANT: Manajan-Miklos, Shalina
APPLICANT: Tan, Man-Wah
APPLICANT: Tan, Man-Wah
APPLICANT: Cao, Hui
APPLICANT: Cao, Hui
APPLICANT: Drenkard, Eliana
APPLICANT: Tsongalis, John
TILLO FINVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REPERENCE: 00786/361002
CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
PRIOR RILING DATE: 1998-11-25
NUMBER OF SEQ ID NOS: 437
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bodie, Elizabeth A.
APPLICANT: Graycar, Thomas P.
APPLICANT: Winerkzky, Deborah S.
TITLE OF INVENTION: Pleurotus Phenol Oxidizing Enzymes FILE REFERENCE: GC57
CURRENT APPLICATION NUMBER: US/09/221,275
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEO ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 12; DB 4; I
100.0%; Pred. No. 1.4e+02;
vative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 12; DB 4; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 12; Conservative 0; Mismatches 0;
                                                RESULT 2
US-09-199-637A-266/c
; Sequence 266, Application US/09199637A
; Patent No. 6355411
                                                                                                                                                                                                     Rahme, Laurence G.
Mahajan-Miklos, Shalina
Tan, Man-Wah
Cao, Hui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09221275 Patent No. 6329332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Borneman, William S.
APPLICANT: Bodie, Elizabeth A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                               Ausubel, Frederick
Goodman, Howard M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: cDNA US-09-221-275-3
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LENGTH: 1341
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LENGTH: 1722
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US-09-221-275-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-221-275-2
Sequence 2, Application US/09221275
Fatent No. 6329332
Fatent Norman William S.
APPLICANT: Bodie, Elizabeth A.
APPLICANT: Graycar, Thomas P.
TITLE OF INVENTION: Pleurotus Phenol Oxidizing Enzymes
FILE REFERENCE: GC557
CURRENT APPLICATION NUMBER: US/09/221,275
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 12; DB 4; Length 20 100.0%; Pred. No. 1.4e+02; ative 0; Mismatches 0; Indels
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APPLICANT: Borneman, William S.
APPLICANT: Borneman, William S.
APPLICANT: Graycar, Thomas P.
APPLICANT: Winetzky, Deborah S.
TITLE OF INVENTION: Pleurotus Phenol Oxidizing Enzymes FILE REFERENCE: GC557
                                                                          GENERAL INFORMATION:
APPLICANT: MOllenhauer, Jan
TITLE OF INVENTION: Protein Containing an SRCR Domain
FILE REPERENCE: 4121-108
CURRENT APPLICATION NUMBER: US/09/341,587
CURRENT FILING DATE: 1999-08 31
EARLIER APPLICATION NUMBER: PCT/DE98/00096
EARLIER FILING DATE: 1988-01-09
NUMBER OF SEQ ID NOS: 12
; Sequence 1, Application US/09221275 ; Patent No. 6329332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Pleurotus ostreatus
US-09-221-275-2
                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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; ORGANISM: Homo sapiens
US-09-341-587-2
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Best Local Similarity
Matches 12; Conserv
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14:
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ATTORNEY/AGENT INFORMATION:
NAMME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3116 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Winter, Robert B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34..2994
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                                                                                                                                                                                                                                       ZIP: 91320
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US-08-702-367A-14
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                                                                                                                                                                                                                   Length 2678;
                                                                                                                                                                                                                                                                                                                                                                                             US-08-449-645A-14/C

| Sequence 14, Application US/08449645A
| Patent No. 2981245
| GENERAL INFORMATION:
| TILLE OF INVENTION: EPH-Like Receptor Protein Tyrosine:
| TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine:
| TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine:
| TITLE OF INVENTION: Alases
| NUMBER OF SEQUENCES: 43
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Amgen Patent Operations/RBW |
| STREET: 1840 Dehavilland Drive |
| COUNTRY: California |
| COUNTRY: USA
                                                                                                                                                                                                             100.0%; Score 12; DB 4; Length 26
100.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZUPORTITE PROBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMENT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
CURRENT APPLICATION NUMBER: US/09/221,275
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 8
SEQ TWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-2
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3116 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                          ; TYPE: DNA
; ORGANISM: Pleurotus ostreatus
US-09-221-275-1
                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 12; Conservative
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LOCATION: 34..2994
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Matches 12; Conserv
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US-08-449-645A-14
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Gaps
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Patent No. 5981246
GENERAL INFORMATION:
APPLICANT: FOX, GAYY M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADRESS:
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TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: 28
CORRESPONDENCE ADDRESS: A
ADDRESSEE: Angen Patent Operations/RBW
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: CALLIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,367A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 100.0%; Score 12; DB 2; L. Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 12; Conservative 0; Mismatches 0;
                                                                                                                                                                        ADDRESSEE: Amgen Patent Operations/RBW STREET: 1840 Dehavilland Drive CITY: Thousand Oaks STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US95/04681
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US95-04681-14/c
; Sequence 14, Application PC/TUS9504681
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 13, Application US/09428711A
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REGISTRATION NUMBER: 00,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 82:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            Genentech, Inc.
Bennett, Brian D.
Goeddel, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELERAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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CLASSIFICATION:
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PCT-US95-04228-34/C
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TOPOLOGY:
PCT-US95-04228-34
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                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
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US-08-222-616-34
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APPLICANT: Goeddel, David
APPLICANT: Goeddel, David
APPLICANT: Atthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Tsai, Siao Ping
APPLICANT: Prosing Rinase AGONIST
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST
TITLE OF INVENTION: ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAPLICATION NUMBER: US/08/222,616
FILING DATE: 4-APR-1994
CLASSIPRICATION: 530
PRIOR APPLICATION NUMBER: PCT/US93/00586
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/826935
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
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REFERENCE/DOCKET NUMBER: 821P2
FELECOMMUNICATION INFORMATION:
TELEPHONE: 415/255-1994
TELEPRAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 34, Application US/08222616 Patent No. 5635177
    REFERENCE/DOCKET NUMBER: A-287 INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
                                                                 LENGTH: 3116 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                LOCATION: 34..2994
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TOPOLOGY: linear
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                                                                                                                                                                                              NAME/KEY: CDS
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APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Fasi, Siao Ping
APPLICANT: Wood, William I.
TITLE OF INVERTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
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Query Match
100.0%; Score 12; DB 1; Length 3348;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
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ET: 460 Point San Bruno Blvd
: South San Francisco
E: California
RRY: USA
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                                                                                                                                                                                                                                                                                               Sequence 34, Application PC/TUS9504228 GENERAL INFORMATION:
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FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
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Query Match
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US-08-254-358-1
; Sequence 1, Application US/08254358
; Patent No. 5658785
; GENERAL INFORMATION:
APPLICANT: Johnson, Philip R.
TITLE OF INVENTION: Methods
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive CITY: Chicago
STREET: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
GENERAL INFORMATION:
APPLICANT: Muramatsu, Masaaki
APPLICANT: Shirasawa, Takuji
APPLICANT: Shirasawa, Takuji
APPLICANT: Shirasawa, Takuji
APPLICANT: Tokumitsu, Hiroshi
APPLICANT: No. 6358720uchi, Teruhisa
TITLE OF INVENTION: SERINE/THREONINE PROTEIN KINASE
FILE REFERENCE: 06501-045001
CURRENT APPLICATION NUMBER: US/09/428,711A
CURRENT FILING DATE: 1999-10-28
PRIOR RILING DATE: 1998-03-23
PRIOR FILING DATE: 1998-03-23
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 21
SOFTWARE FASTESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,358
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 12; DB 4; I
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0;
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ATORNEY/AGENT INFORMATION:
NAME: NO. 5568785and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/POCKET NUMBER: 31975
TELEPHONE: (312) 474-6300
TELEPAX: (312) 474-6300
TELEPAX: (312) 474-6300
TELERAX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1)...(3995)
; OTHER INFORMATION: n = A,T,C or G
US-09-428-711A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: CDS
LOCATION: (388)...(3540)
NAME/KEY: misc_feature
NAME/KEY: '...
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2875 CAGGAGCCTCGA 2864
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Mus musculus
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LENGTH: 3995
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                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-08-475-391-1
; Sequence 1, Application US/08475391
; Patent No. 5786211
; GENERAL INFORMATION:
APPLICANT: Johnson, Philip R.
TITLE OF INVENTION: Methods
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                        ö
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                                                                                                                                                                              100.0%; Score 12; DB 1; Length 4680; 100.0%; Pred. No. 1.4e+02;
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                                                                                                                                                                                                                      Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: ELBM PC compatible
COMPOTER: IEM PC compatible
COMPOTER: TEM PC compatible
COMPOTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,391
FILING DATE: 07-JUN-1995
CLLASSIFICATION: DATA:
APPLICATION NUMBER: 08/254,358
FILING DATE: NUMBER: 08/254,358
FILING DATE: NUMBER: 3392
FILING DATE: NUMBER: 3392
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (312) 474-6300
TELERAX: (312) 474-6300
TELERAX: SSOIDS SEQIED NO: 1:
SROHENTER SEQIED NO: 1:
                                                                                                                                                                                                                        0; Mismatches
LENGTH: 4680 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-254-358-1
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MOLECULE TYPE: DNA (genomic)
US-08-475-391-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 4680 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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Matches 12; Conservative
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GENERAL INFORMATION:
APPLICANT: Johnson, Philip R.
TITLE OF INVENTION: Adeno-Associated Virus Materials and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                   ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILINO JATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5688775and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31975
TELEPOMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELERAX: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4680 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                ; Sequence 1, Application US/08709609
; Patent No. 5858775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-709-609-1
                                                                                                                                                                                                                                                                           CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
US-08-709-609-1
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Query Match 100.0%; Score 12; DB 2; Length 4680; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 12; Conservative 0; Mismatches 0; Indels 0

1 caggageetega 12 ŏ

Search completed: July 31, 2002, 12:23:49 Job time: 11852 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

July 31, 2002, 12:12:05; Search time 5855.71 Seconds (without alignments) 27.659 Million cell updates/sec Run on:

US-09-899-718A-6 12 Title: Perfect score:

1 caggageetega 12 Sequence:

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

13736207 seqs, 6748477542 residues

Searched:

27472414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 08 Maximum Match 100%

EST:* Database :

em_estba:*

gb_gss:* em_gss_hum:* em_gss_inv:* em_gss_pln:* em_gss_vrt:* em_esthum: *
em_estin: *
em_estin: *
em_estov: *
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em_estro: *
em_htc: *
gb_est1: *
gb_est2: *
gb_htc: * 10: 111: 113:::14: 115::15:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

BF371310 RC6-FN011
AZ747991 RPC1-24-1
BH354246 CH230-680
AZ748898 RPC1-24-1
AA584951 nn41b12.s
B1518243 603042090
BF812758 CM2-C1018
BF926690 PMI-NT023
BE827454 CM2-FT001
B1002833 MR3-HN016 AZ271167 RPCI-23-4 AV640236 AV640236 AA038245 mi82e03.r AA074114 zf79f05.r AA657774 nu06f04.s BB552607 BB592607 AA770456 aN89f12.s Description SUMMARIES AZ747991 BH354246 AZ748898 AA584951 B1518243 BF812758 BF926690 BE827454 B1002833 AZ271167 AV640236 AA038245 AA074114 AA657774 BB592607 AA770456 G Query Match Length DB 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 Score Result . Q 10 11 12 11 13 11 14 11 11 11 11

AA450935 vf85b01.r BB588724 BB588724 BE091664 IL2-BF073 BF605617 272154 MA BM054775 E88504.x BG775999 NXST 147	BB354103 BB354103 B1051362 RC5-GN028 D21628 MB375D04 mc BE838749 RC6-FN011 BF402808 UI-R-CA0- BH204013 SMI-46514 BM068805 1e85c04.y		BE143676 MRO-HT016 BI008774 QV3-RT006 AA348160 EST54567 AA365578 EST76401 BB590276 BB590276 A1564849 tm66a06.x AW325543 17495 MAR R22443 yA23906.s1
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1000.0 1000.0 1000.0	1000.0000000000000000000000000000000000	100.0 100.0 100.0 100.0	12 1000.0 12 1000.0 12 1000.0 12 1000.0 12 1000.0 12 1000.0 13 1000.0 14 1000.0 15 1000.0 16 1000.0 17 1000.0 17 1000.0 17 1000.0
0 0 118 0 20 0 20 0 23	100000000	0 32 334 34 34 37	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

ALIGNMENTS

BF371310 RC6-FN0114-090800-011-E11 FN0114 Homo sapiens CDNA, mRNA sequence. BF371310 BF371310.1 GI:11333244 EST. human.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 109) Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Coldman,G.H., Carvalho,A.F., Matsukuma,A., Balai,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and	Simpson, A.J. Shotgun sequencing of the human transcriptome with ORF expressed sequence tags Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Brazil Tel: +55-11-2700401 Fax: +55-11-2707001 Fax: +55-11-2707001 Fax: point a simpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project: This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=RC66t2=RC6-FN0114-090800-011-Ellts-2000-08-095t4=1) Seq prime: puc. 18 forward High muality sequence start: 3%	
RESULT 1 BF371310/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL	COMMENT	FEATURES source

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Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
                                                                                                                                                                                                                                                                                                  GSS 03-DEC-2001
                                                                                                                                                                                                                                                                                                                CH230-68019.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-68019, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="Brain"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SSNHSd/MCW) BAC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html Plate: 68 row: 0 column: 19
                                                                                                Gaps
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                                                 Length 110;
                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                 100.0%; Score 12; DB 12; 100.0%; Pred. No. 8.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="CHORI-230 Segment 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
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                                                                                             0; Mismatches
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The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                118 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="CH230-68019"
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                                                                                                                                                                                                                                                                                                                                                                                         BH354246.1 GI:17284980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 118)
                                            Query Match
Best Local Similarity 100.0
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             norvegicus
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                                                                                                                                        1 caggageetega 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Norway rat.
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                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                           BH354246/c
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                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end page: http://www.chori.org/bacpac/orderingframe.htm). BAC end Plate: 125 row: D column: 2 bac_ends/mouse/bac_end_intro.html Seq primer: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RFCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
Russell,D., de Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ747991 110 bp DNA linear GSS 25-JAN-200:
RPCI-24-125D2.TV RPCI-24 Mus musculus genomic clone RPCI-24-125D2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 110)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clones are derived from the mouse BAC library RPCI-24. For BAC
                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                100.0%; Score 12; DB 10; Length 109; 100.0%; Pred. No. 8.6e+03; ative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse BAC End Sequences from Library RPCI-24 Unpublished (1999)
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/clone_lib="RPCI-24"
/db_xref="taxon:9606"
/clone_lib="FN0114"
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                                            /dev_stage="Adult"
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AZ748898 125F2.TV RPCI-24 Mus musculus genomic clone RPCI-24-125F2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 125 row: F column: 2
Seq primer: T7
Class: BAC ends.
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RRCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
DNA."
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Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other,GSSs: RPCI-24-125F2.TJ
Contact: Shaying Zheo
Department of Eukaryotic Genomics
The Institute for Genomic Research
Tel: 301 838 0200
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 133)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/clone="RPCI-24-125F2"
/clone_lib="RPCI-24"
/sex="Male"
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/clone_lib="NCI_CGAP_GC5"
/clone_lib="NCI_CGAP_GC5"
/tlssue_type="germ cell tumor"
/tlssue_type="germ cell tumors"
/tlssue_type="g
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                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
DNA Griduation: NCL-CGAP clone distribution information can be found through the LLM.A.G.E. Consortium/LLNL at:
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I (bases 1 to 1414)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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Contact: Robert Strausberg, Ph.D.
Email: Gapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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plate: LLAM11455 row: c column: 24
High quality sequence start: 24
High quality sequence stop: 144.
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
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/db_xref="taxon:9606"
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source

FEATURES

BASE COUNT ORIGIN

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Gaps ; EST 19-JAN-2001

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/note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMl&t2=PMl-NT0235-011200-002-al0&t3=2000-12-01&t4=1)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 153)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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High quality sequence start: 13
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pCNV-SPORT6: Site_1: NotI: Site_2: ECCRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (ECCRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1.3 kb. Library is normalized and
enriched for full-length clones and was constructed by C
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
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CM2-CI0180-221100-540-b07 CI0180 Homo sapiens CDNA, mRNA sequence.
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., Gardin, S., Costa, F.F., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Seq primer: puc 18 forward
High quality sequence start: 24
High quality sequence stop: 144.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Location/Qualifiers
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Fax: +55-11-2707001
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?tl-&t2-CM2-ET0016-310
Seq primer: puc 18 forward
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Shotgun sequencing of the human transcriptome with ORF expressed
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509–010, Sao Paulo-SP,
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Contact: Erika Asamizu
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                                                                                                                                                                      /strain="C9"
                                                                                                                                                                                                                                                                                                                          dioxide"
a 56 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.0
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AV640236 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii 5% AV640236 Chlamydomonas reinhardtii 4V640236
                                                                                  zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia! Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 176)
                                                                                                                                                                                                                                                                                                                                                                    library availability, please contact Pieter de Jong
(pieterédejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakamura, Y. and Tabata, S.
Generation of expressed sequence tags from low-CO2 and high-CO2 adapted cells of Chlamydomonas reinhardtii
DAR Res. 7 (5), 305-307 (2000)
                                                                                                                                                                                                                                                                                                                          Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 444 row: J column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with a combination of EcoRI and EcoRI Methylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 12; DB 12; Length 176; 100.0%; Pred. No. 9.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                             The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0208
                                                                                                                                             Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 t
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                                                                                                                                                                                                                    Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
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/clone="RPCI-23-444J17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _lib="RPCI-23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="C57BL/6J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Female"
                                                                                                                                                                                             Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 177)
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Mus musculus
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Best Local Similarity
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                                                                                      AUTHORS
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/dev_stage="19.5 dpc total fetus"
/lab_host="0H10B (ampicillin resistant)"
/note="Vector: pT73D (pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kasarau, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                         /clone_lib-"Chlamydomonas reinhardtii 5% CO2"
/note="Vector: pBluescriptII SK; Site_1: EcoRI; Site_2:
Xhoi; The cDNA library was constructed from cells cultured
in a medium with bubbling air containing 5% carbon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 186)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST 28-AUG-1996
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 bp mRNA linear EST 28 mi82e03.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:473116 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                   /organism="Chlamydomonas reinhardtii"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 12; DB 9; L 100.0%; Pred. No. 9.8e+03;
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Washington University School of MedicineP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
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                                                                                                                                                                                                                                                           /db_xref="taxon:3055"
                                                                                                                                                                                                                                                                                              /clone="HCL012f11_r"
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us-09-899-718a-6.rst

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Anote—"Vector: pawplo; site_1: Not1; Site_2: EcoRI; lst strand cDNA was primed with oligo(d7)17 on 50 mg of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdisseted prenceplastic cells histologically-determined to be prostatic intrapplithelial neoplasia 2 (PIN2) cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the CDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pample 0 the updc-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-remail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.,
Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrapada by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                   AA657774 1106ar EST 05-NOV-1997 nu06£04.s1 NCI_CGAP_Pr2 Homo sapiens CDNA clone IMAGE:1207231, mRNA
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 198)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:1207231"
/clone_lib="NCI_CGAP_Pr2"
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/lab_host="DH10B"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: July 31, 2002, 12:12:09 Job time: 13482 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 100.

Best Local Similarity 100.

Matches 12; Conservative
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                              1 caggageetega 12
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AA657774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 193)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hullman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rikin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Materston,R., Williamson,A., Wohldmann,P. and Wilson,R.

Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 07-0CT-1996
double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 177.
                                                                                                                                                                                                                                                                                                                           Gaps
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Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                        100.0%; Score 12; DB 9; Length 186; 100.0%; Pred. No. 1e+04; Live 0; Mismatches 0; Indels
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/db_xref="GDB:1291426"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Listing first 45 summaries
                                                                                                                                    OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS1/gcgdata/hold-geneseg/genesegn-embl/NA2001A.DAT:*/SIDS1/gcgdata/hold-geneseg/genesegn-embl/NA2001B.DAT:*/SIDS1/gcgdata/hold-geneseg/genesegn-embl/NA2002.DAT:*

			Description	ni Das remine DCR orimer see din	Oligonucleotide #2	Human albumin (HA)	Human albumin (HA)	Human albumin (HA)	Human bone marrow	Drosophila melanog	Human secreted pro	Eucalyptus grandis
SUMMARIES			ID	AAT63580	ABA03059	AAD22289	AAD21640	AAD20007	AAK51355	ABL27525	AAC31784	AAA69618
			83	18	22	22	22	22	22	23	21	21
			e Match Length DB I	32	28	59	29	59	193	261	292	315
	ф	Query	Match 1	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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Sharma A;

Logan JS,

Byrne GW, Diamond LE, WPI; 1997-225881/20

	STITINGFILL						
DNA encoding novel	Ξ	23	3342	100.0	12	45	U
Human ORFX ORF1964	2	21	3197	100.0	12	44	
EPH-like receptor	AAT02948	16	3116	100.0	12	43	O
DNA encoding novel	AAS69876	23	3107	100.0	12	42	O
Human cDNA sequenc	319	22	2993	100.0	12	41	
	43	21	2678	100.0	12	40	
sed	AAA57400	21	2678	100.0	12	39	
Drosophila melanog	ABL09501	23	2674	100.0	12	38	D
Genomic sequence o	AAA57438	21	2671	100.0	12	37	
	AAA57401	21	2671	100.0	12	36	
	AAH15967	22	2305	100.0	12	32	υ
	ABL27524	23	2261	100.0	12	34	
	AAV49651	19	2000	100.0	12	33	O
ducin 44	AAH76656	22	1947	100.0	12	32	O
CDNA Sequence enco	AAA57439	1.5	1722	100.0	12	3.5	
Eucalyptus grandis	AAA69617	7.5	1722	100.0	12	5 7 6	O
Drosophila melanog	ABL23803	23	1563	100.0	12	28	
Arabidopsis thalia	AAC33226	21	1527	100.0	13	27	
Nucleotide sequenc	AAX98114	20	1341	100.0	12	56	Ö
Eucalyptus grandis	AAA69541	21	1271		12	25	O
Ripening banana pu	AAV28653	19	822	100.0	12	24	υ
Human pancreatic c	AAC99009	21	697		12	23	ပ
Murine 7-transmemb	AAH97769	22	652		12	22	υ
	AAH97771	22	647		12	21	υ
Murine 7-transmemb	AAH97773	22	633		12	20	O
Human secreted exp	AAA43765	21	616		12	19	
Human bone marrow	AAK38542	22	582		12	18	
Human cDNA clone (AAH10794	22	568		12	17	
7	AAH97770	22	559		12	16	υ
Murine 7-transmemb	AAH97774	22	552		12	15	O
Secreted protein E	AAZ40844	20	475		12	14	O
Aloe arborescens p	AAT74033	18	450		12	13	
Human secreted pro	AAC08874	21	400		12	12	ບ
	AAC04396	21	394		12	11	
Human ORFX ORF1296	AAC75741	21	341		12	10	υ

ALIGNMENTS

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Xenotransplantation; organ transplant; transgenic animal; transgenic pig; transgenic mouse; antibody mediated rejection; hyperacute rejection; CD59; complement inhibitor; primer; PCR; polymerase chain reaction; minigene; ss.
                                                                           PCR primer used in CD59 minigene No. 1 construction.
                  AAT63580 standard; DNA; 32 BP
                                                                                                                                                                                                      96WO-US15255
                                                                                                                                                                                                                         96US-0675773
95US-0004461
                                                          (first entry)
                                                                                                                                                                                                                                                      (NEXT-) NEXTRAN.
                                                                                                                                                               W09712035-A2
                                                                                                                                                                                                      23-SEP-1996;
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27-SEP-1995;
                                                                                                                                                                                   03-APR-1997.
                                                         01-JUL-1997
                                                                                                                                             Synthetic.
                                    AAT63580;
          AAT63580/c
RESULT
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0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       serum albumin; HA; antiinflammatory; immunosuppressive; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to albumin fusion proteins, which comprise
                                                                                                        A sense primer (AAT63579) and antisense primer (AAT63580) were designed to amplify a 1033 bp sequence of the 3' flanking region of the human CD59 gene, with the introduction of a 5' SacI site and 3' XhoI site. The PCR product was joined to CD59 cDNA contg. exons 2, 3 and 4 plus 667 bp of 3' untranslated region (see also AAT63577-78)
Transgenic animals expressing antigen reducing enzyme and complement inhibitor - used for production of materials suitable for human transplantation having a reduced risk of rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Albumin fusion proteins comprising a therapeutic protein and albumin, useful in the treating immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction) and hyperproliferative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                              to produce a CD59 minigene. This minigene was shown to retain biological function when expressed in transgenic pigs and mice. Expression of a complement inhibitor such as CD59 on endothelial
                                                                                                                                                                                                                                                    cells of transgenic animals can provide materials suitable for transplantation to humans, suppressing complement activation and
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                                                                                                                                                                                                                                                                                                                                                                                   Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide #2 used to construct a HA fusion sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 12; DB 18; 100.0%; Pred. No. 8.9e+02;
                                                                                                                                                                                                                                                                                                                             Sequence 32 BP; 3 A; 9 C; 11 G; 9 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                      Example 1.1; Page 64; 146pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-APR-2000; 2000US-229358P.
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2000US-256931P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                           reducing immune reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Best Local Similarity
Matches 12; Conserv
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21-DEC-2000;
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In the treatment, prevention, diagnosis, and/or detection of diseases/disorders such as immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction), hyperproliferative disorders (e.g. childhood acute myeloid leukemia), renal disorders (e.g. childhood acute myeloid leukemia), arrhythmias), respiratory disorders (e.g. non-allergic finitiis), neurological diseases (e.g. Lizheimer's disease), endocrine disorders (e.g. pheocytochroma), reproductive system disorders (e.g. syphilis), infectious diseases (e.g. measles), gastrointestinal disorders (e.g. inrealle bowel syndrome) and wound healing. In the present invention, human serum albumin (HA; see AAM52567) was used to generate fusion
                                                                                                                                                                                                                                                                                                                                                                                     ö
therapeutic protein and albumin. The albumin fusion proteins are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to albumin fusion proteins comprising therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; albumin; HA; fusion protein; immune system disorder; syphilis; transplant rejection; blood related disorder; myocardial infarction; hyperproliferative disorder; acute myelold leukaemia; renal disorder; glomerulonephitis; cardiovascular disorder; arrhythmia; rhinitis; respiratory disorder; neurological disease; Alzheimer's disease; endocrine disorder; phecoytochroma; reproductive system disorder; measles; gastrointestinal disorder; irritable bowel syndrome; HIV; human immunodeficiency tirus; wound healing; renal cell carcinoma; melanoma; gene therapy; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Albumin fusion proteins comprising a therapeutic protein and albumin, useful in the treating metastatic renal cell carcinoma, metastatic melanoma, malignant melanoma, renal cell carcinoma, HIV (human
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                           proteins. The present sequence was used to illustrate the invention.
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                                                                                                                                                                                                                                                                                                                                           100.0%; Score 12; DB 22; Length 58; 100.0%; Pred. No. 8.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                Sequence 58 BP; 13 A; 15 C; 12 G; 18 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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ID AAD22289 standard; DNA; 59 BP.
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25-APR-2000; 2000US-199384P.
21-DEC-2000; 2000US-256931P.
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                        1 caggageetega 12
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                                                                                                                                                                                                                                                                                                                                             Query Match
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protein and human albumin (HA). The albumin fusion proteins are useful in the treatment, prevention, diagnosis, and/or detection of diseases, disorders such as immune system disorders (transplant rejection); blood related disorders (myocardial infarction); hyperproliferative disorders (childhood acute myeloid leukaemia); renal disorder (glomerulonephritis); candidovasular disorders (arrhythmias); respiratory disorders (non-allergic rhinitis); neurological diseases (Alzheimer's disorders (syphilis); infectious diseases (measles); gastrointestinal disorders (syphilis); infectious diseases (measles); gastrointestinal disorders (srphilis); infections diseases (measles); gastrointestinal disorders (irritable bowel syndrome) and wound healing. The albumin fusion proteins are also used in the treatment of metastatic renal cell carcinoma, metastatic melanoma, malignant melanoma and HIV (human protein used for engineering the Xho and Cla I restriction sites (into the DNA encoding HA protein in pepto006 plasmid.

Conto the DNA encoding HA protein in pepto006 plasmid.

Note: The present sequence shown in sequence listing of the specification can be at its 3' end.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Albumin fusion proteins comprising a therapeutic protein and albumin, useful in the treating immune system disorders (e.g. transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 59 BP; 13 A; 16 C; 12 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 12; DB 22; 100.0%; Pred. No. 8.9e+02;
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 caggageetega 12
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The invention relates to albumin fusion proteins comprising therapeutic protein and human albumin (HA). Therapeutic protein fused to albumin thave an extended shelf-life. The albumin fusion proteins are useful in the treatment, prevention, diagnosis and/or detection of diseases, disorders such as immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction), hyperproliferative disorders (e.g. childhood acute myeloid leukaemia), renal disorders (e.g. qlomerulonephritis), cardiovascular disorders (e.g. arrhythmias), respiratory disorders (e.g. non-allergic rhinitis), neurological pheocytochroma), reproductive system disorders (e.g. syphilis), infectious diseases (e.g. massles), gastrointestinal disorders (e.g. infiritable bowel syndrome) and wound healing. Nucleic acids encoding them is the syndrome of the sy
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rejection), blood related disorders (e.g. myocardial infarction) and hyperproliferative disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      albumin fusion protein is used in gene therapy. The present sequence is a PCR primer used for engineering the Xno and Cla I restriction sites into the DNA encoding HA protein in pPPC0006 plasmid. Note: This sequence SEQ.ID.NO.20 is stated to be similar to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence shown in the sequence listing. However this sequence contains an additional base 'C' at the 3' end which is absent in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the sequence shown in sequence listing.
                                                                                               Example 2; Page 231; 380pp; English.
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2000US-199384P.
2000US-256931P.
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Best Local Similarity
Matches 12; Conserv
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25-APR-2000;
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corresponding nucleic acid sequences. Therapeutic proteins and their corresponding nucleic acid sequences. Therapeutic proteins fused to corresponding nucleic acid sequences. Therapeutic proteins fused to dispanses have an extended shelf-life. The albumin of fusion proteins are useful in the treatment, prevention, diagnosis, and/or detection of diseases, disorders such as immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction), hyperproliferative disorders (e.g. childhood acute myeloid leukaemia, metastatic renal cell carcinoma, metastatic metastatic renal cell carcinoma, metastatic metastatic spiral disorders (e.g. arrhythmias), cegin giomerulonephritis), cardiovascular disorders (e.g. arrhythmias), respiratory disorders (e.g. non-allergic rhinitis), neurological diseases (e.g. Alzheimer's diseases), endocrine disorders (e.g. syphilis), diseases (e.g. non-allergic rhinitis), neurological diseases (e.g. Alzheimer's diseases), measles), gastrointestinal disorders (e.g. infections diseases (e.g. non-allergic rhinitis), cardiome), HIV (human immunodeficiency virus) infection and wound healing. Nucleic acids encoding albumin fusion protein is used for engineering the Xho and Cla I restriction sites into the fusion leader sequence 1sts for of the DNA encoding the HA protein in pPPC0006 plasmid.

Chote: This sequence SPQ.ID.No.20 is stated to be similar to the sequence shown in the sequence listing. However this sequence contains an additional base (C. at the 3 end which is absent in
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                                                                                                                                                                                                                                           invention relates to human albumin (HA) fusion proteins and their
                                                                                              Albumin fusion proteins comprising a therapeutic protein and albumin, useful in the treating metastatic renal cell carcinoma, metastatic melanoma, malignant melanoma, renal cell carcinoma, HIV (human
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Pred. No. 8.9e+02;
Mismatches 0;
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                                                                                                                                                               immunodeficiency virus) or infection
                                                                                                                                                                                                 Example 2; Page 244; 394pp; English.
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
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Best Local Similarity 100.
                  Haseltine WA;
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                  Rosen CA,
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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                           The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster genomic polynucleotide SEQ ID NO 34048.
                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                Example 4; SEQ ID NO: 25912; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                             Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 34048; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                Sequence 193 BP; 32 A; 47 C; 27 G; 87 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 12; DB 22; 100.0%; Pred. No. 8.8e+02;
                                                                                                                                                                                   analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myers EW;
                                                                                                         Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                          (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Li PWD,
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                      the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL27525 standard; DNA; 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2000; 2000US-191637P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmaceutical; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster.
                                                                                                        Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 caggageetega 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 caggageetega 74
                                                                                                                                      WPI; 2001-488900/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL27525;
                                                                                                         Penn SG,
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                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
              and
                                                                                                                                                                                                                                                                                                                                                                Gaps
useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                 Length 261;
                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                     Sequence 261 BP; 83 A; 66 C; 68 G; 44 T; 0 other;
                                                                                                                                                                                                                                                                                                          100.0%; Score 12; DB 23; 100.0%; Pred. No. 8.8e+02;
                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         109 caggageetega 120
                                                                                                                                                                                                                                                                                                                                                                                                       1 caggageetega 12
                                                                                                                                                                                                                                                                                                            Query Match
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Human secreted protein 5' EST, SEQ ID NO: 35859. gene therapy; chromosome mapping; ss. AAC31784 standard; cDNA; 292 BP (first entry) Human; 5' EST; 06-OCT-2000 AAC31784; AAC31784/c NAMES OF COLOR OF COL

expressed sequence tag; secreted protein; cDNA isolation; Homo sapiens.

EP1033401-A2 06-SEP-2000. 21-FEB-2000; 2000EP-0200610

99US-0122487 26-FEB-1999;

(GEST) GENSET

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures Dumas Milne Edwards J, Duclert A, Giordano J; WPI; 2000-500381/45.

Claim 1; SEQ ID 35859; 71pp + CD-ROM; English

The present sequence is one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTS are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. Se ESTS are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTS are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. expression and secretion vectors.

Sequence 292 BP; 63 A; 76 C; 73 G; 80 T; 0 other;

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                                                                                                                                                                                                      Eucalyptus grandis: Pinus radiata; modification; isoprenoid; plant; metabolism; isoprenoid blosynthetic pathway; terpenoid; steroid; genome mapping; physical mapping; postitional cloning; forestry; agriculture; medicine; fermentation; plant development; pest resistance;
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New plant polynucleotides encoding polypeptides involved in the production and modification of isoprenoids, useful in forestry and agriculture for manipulation of isoprenoid metabolism -
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  Length 292;
                     Indels
                      ..
100.0%; Score 12; DB 21; 100.0%; Pred. No. 8.8e+02;
                     0; Mismatches
                                                                                                                                                                                   Eucalyptus grandis NADPH cDNA SEQ ID NO:92.
                                                                                                                                                                                                                                                                                                                                                                                          (GENE-) GENESIS RES & DEV CORP LTD.
(FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                                                                   pinene; myrcene; Monterey pine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 82; 164pp; English.
                                                                                                                   AAA69618 standard; cDNA; 315 BP
                                                                                                                                                                                                                                                                                                                                       99WO-NZ00219.
                                                                                                                                                                                                                                                                                                                                                           98US-0215504
99US-0146441
                                                                                                                                                             (first entry)
                      Conservative
                                                       222 CAGGAGCCTCGA 211
                                          1 caggageetega 12
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-431575/37.
                                                                                                                                                                                                                                                                       Eucalyptus grandis.
          Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAB18018
                                                                                                                                                                                                                                                                                            WO200036081-A2.
                                                                                                                                                                                                                                                                                                                                     16-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                          Havukkala IJ;
                                                                                                                                                                                                                                                                                                                                                          17-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                    29-JUL-1999;
                                                                                                                                                             08-NOV-2000
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  Query Match
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The present invention describes plant polynucleotides encoding polypeptides involved in the production and modification of isoprenoids, such as terpenoid and steroid compounds. The polynucleotides are used in genome mapping, in physical mapping and in positional cloning of an including containing and in positional cloning of agriculture for manipulation of isoprenoid metabolism, in medicine for therapeutic effects, including direct application in diseased organisms or indirect application by transgenic organisms and in fermentation and chemical processing industries involving isoprenoids. In plant capplications, manipulating isoprenoid pathways or isoprenoid composition may, for example, affect plant development, pest resistance, and the value of extractives (e.g. pinene and myrcene). The ubiquitous and contained roles of isoprenoids make the polynucleotides attractive targets for biotechnical applications in a variety of fields. AAA69527 to AAA69690 and AAB18004 to AAB18143 represent Eucalyptus grandis and Pinus contained the advance of the contained and proteins used in the exemplification of the invention present

Sequence 315 BP; 77 A; 96 C; 90 G; 52 T; 0 other;

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antidiabetic; hypotensive; dermatological; immunosippressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORRX-associated disorder. The nucleic acids can be used to express ORRX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                  Human, open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosupressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antilnflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acids and peptides derived from open reading frame \mathbf{X},
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
                                         0
100.0%; Score 12; DB 21; Length 315; 100.0%; Pred. No. 8.8e+02;
                                                                                                                                                                                                                                                                                                                                                            Human ORFX ORF1296 polynucleotide sequence SEQ ID NO:2591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for treating e.g. cancers, proliferative disorders,
                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurodegenerative disorders and cardiovascular disease
                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; Page 1852; 5507pp; English.
                                                                                                                                                                                                                                     AAC75741 standard; cDNA; 341 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombosis; contraceptive; ss.
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99US-0127636.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-2000; 2000US-0540763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000; 2000WO-US08621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0127728
                                                                                                                                                                                                                                                                                                                     08-FEB-2001 (first entry)
                                         12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shimkets RA, Leach M;
                                                                                                                             120 CAGGAGCCTCGA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CURA-) CURAGEN CORP.
                                                                                      1 caggageetega 12
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                      Best Local Similarity
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                                                                                                                                                                                                                                                                               AAC75741;
Query Match
                                         Matches
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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences dare been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autcimmune disorders, astima, allegies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -
                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                      100.0%; Score 12; DB 21; Length 341; 100.0%; Pred. No. 8.8e+02;
                                                                                                                                                    coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                           Sequence 341 BP; 74 A; 82 C; 125 G; 60 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dumas Milne Edwards J, Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted protein 5' EST, SEQ ID NO: 8471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID 8471; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy; chromosome mapping; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC04396 standard; cDNA; 394 BP.
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                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  267 CAGGAGCCTCGA 256
                                                                                                                                                                                                                                                                                                                                             1 caggageetega 12
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                                                                                                                                                                                                                                                                                                                                                           Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
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100.0%; Score 12; DB 21; Length 394; 100.0%; Pred. No. 8.8e+02; ative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                      Human secreted protein 5' EST, SEQ ID NO: 12949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dumas Milne Edwards J, Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID 12949; 71pp + CD-ROM; English.
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                                                                                                                                                                                                   AAC08874 standard; cDNA; 400 BP.
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                                                                                                                                                                                                                                                                                 (first entry)
                   Local Similarity 100.
Les 12; Conservative
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nes 12; Conservative
                                                                                                         117 caggagcctcga 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                       Human; 5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP1033401-A2
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                                                                                                                                                                                                                                                                                 06-OCT-2000
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                                                                                                                                                                                                                                            AAC08874;
   Query Match
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Matches
                                     Matches
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RESULT

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chromosome mapping; human; hereditary disease; diagnosis; cancer; hyperlipidaemila; oardiovascular; neurodegenerative disorder; therapy; autoimmune disease; rheumatic disease; embryogenic disorder; myopathy; renal injury; amino aciduria; hypoglycaemia; male rat infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a probe for phosphoenolpyruvate carboxylase (PEPCase) from Aloe arborescens. A plasmid containing the DNA sequence of PEPCase can be introduced into a monocotyledonous plant to enhance PEPCase activity. The transformed plant has a high ability to fix carbon dioxide under dry conditions. It can also increase corn productivity when introduced into a corn plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phospho:enol:pyruvate carboxylase gene of a monocotyledonous CAM plant - used to transform plants so that they can fix carbon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                      PEPCase; monocotyledonous CAM plant; carbon dioxide fixation; transformation; polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 12; DB 18; Length 450; 100.0%; Pred. No. 8.8e+02; ive 0; Mismatches 0; Indels (
                                                                                                                                            Aloe arborescens phosphoenolpyruvate carboxylase probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Secreted protein; fingerprint identification technique;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Secreted protein EST coding sequence 78-6-2-B10-FL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 450 BP; 96 A; 101 C; 147 G; 106 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 10; 12pp; Japanese.
AAT74033 standard; cDNA; 450 BP.
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ID AAZ40844 standard; DNA; 475 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MITK ) MITSUI TOATSU CHEM INC
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                              Aloe arborescens.
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                                                                                                                                                                                                                                                                                                           JP09107975-A
                                                                                                                                                                                                                                                                                                                                                                                                      19-OCT-1995;
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                                              AAT74033;
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This sequence encodes a human secreted protein of the invention. The extended cDNAs (or genomic DNAs obtainable from them) may be used to prepare PCR primers and probes. These are useful for forensic matching or positive identification by DNA sequencing. They may also be used in alternative fingerprint identification techniques. Antibodies against the proteins encoded by the extended cDNAs are useful in identification of tissue types or cell species, as well as identifying tissue specific soluble proteins. The sequences can be used for chromosome mapping and identification of genes associated with hereditary diseases or drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                response. signal sequences from the construction of secretion vectors. Other sequences derived from the extended cDNAs can be used to clone upstream genomic DNA sequences including promoters. This is in turn useful for identifying proteins that interact with promoter sequences. Some of the proteins may be useful in diagnosing and treating several disorders including, but not limited to: cancer, hyperlipidaemia, cardiovascular and neurodegenerative disorders, autoimmune diseases, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rheumatic diseases, embryogenic disorders, hypertension, renal injury, amino acidurias, hypoglycaemia, male rat infertility and myopathies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine 7-transmembrane G-protein coupled receptor coding sequence #18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                Extended cDNAs useful for expressing secreted proteins and to obtain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine, hematopoietic stem cell; signalling; vaccine; 7TM-GPCR; 7-transmembrane G-protein coupled protein receptor; ds.
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                                                                                                                                                                      Bougueleret L, Duclert A, Dumas Milne Edwards J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                       Claim 1; Page 224-225; 244pp; English.
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ID AAH97774 standard; DNA; 552 BP.
                                                            98US-0081563.
98US-0096116.
98US-0099273.
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                                               98US-0074121.
           99WO-IB00282.
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                                                                                                                                                                                                                                                                                    specific antibodies
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                        (GEST ) GENSET
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             09-FEB-1999;
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Indels

100.0%; Score 12; DB 22; Length 552; 100.0%; Pred. No. 8.8e+02;

0; Mismatches

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7-transmembrane G-protein coupled protein receptors (TTM-GPCRs). The present sequence is one such murine 7TM-GPCR coding sequence. The present sequence was derived from hematopoietic stem cells. The present sequence and its corresponding protein are useful in the prevention, diagnosis and treatment of diseases associated with inappropriate 7TM-GPCR expression. TYM-GPCRs identify specific signalling molecules, to activate an effector-signalling cascade that triggers an intracellular response and eventually a biological effect.
                                                                                                                                                                                                                                                                                              DNA Sequences encoding 7-transmembrane G-protein coupled protein receptors characteristic of hematopoietic stem cells, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to murine coding sequences for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 552 BP; 126 A; 120 C; 125 G; 95 T; 86 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 30-31; 176pp; English.
                                                                                                                                 Pereira DS;
(IMCL-) IMCLONE SYSTEMS INC.
                                                                                                                                 Lemischka IR, Witte L,
                                                 UNIV PRINCETON
                                                                                                                                                                                                                  WPI; 2001-522596/57
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AX349068 Sequence AF150645 Petrotyx AF150652 Mastacemb AF084320 Tamarix s G49233 DIErtd754e E12962 cDNA encodi Z79832 H.sapiens c AR17408 Sequence ARD20839 Homo sapi G39052 Z11764 Zebr

AF321195 Unculture M36196 Human synap G41958 SHGC-68982

A70150 Sequence 11 293109 M.acuminata Ac083094 Clardia 1 Ac076609 Glardia 1 Ac085805 Glardia 1 Ac085805 Glardia 1 Ac087176 Glardia 1 Ac07174 Glardia 1 Ac07774 Glardia 1 Ac07777 Glardia 1 Ac07777 Glardia 1 Ac085377 Glardia 1 Ac08537 Glardia 1

Minimum DB seq Maximum DB seq

Database

Title: Perfect score:

Sequence:

OM nucleic

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Scoring table:

Searched:

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synthetic construct.
synthetic construct
artificial sequence.
1 (sites)
Sprunck,S., Kluth,A., Becker,D., Luetticke,S. and Loerz,H.
Promoters of gene expression in plant caryopses
Patent: WO 0202785-A 6 10-JAN-2002;
Aventis CropScience GmbH (DE)
Location/Qualifiers
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/organism="synthetic construct"
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Sequence 6 from Patent W00202785.
Ax349068 1G::18615103
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HBHWGRZM
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AC062911
AC082911
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AC038729
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AC071714
AC066979
AC085377
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OVU53517
OHU53519
AC043716
AC086493
AC060381
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AC065036
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AC054357
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AC057542
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HUMSYB1A1
                   TSITSAA1
G49233
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HS301F5
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JOURNAL
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AX349068
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                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
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KEYWORDS
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                                          July 31, 2002, 14:01:53; Search time 6034.22 Seconds (without alignments) 41.616 Million cell updates/sec
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                                                                                                                                      3595312
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     GenCore version 4.5 Copyright (c) 1993 - 2000 Comp
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LOCUS G49233 442 bp mRNA linear STS 31-AUG-1999 DEFINITION DIErtd754e Mouse eight-cell stage embryo cDNA library (M. Ko) Mus
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Tamarix sp. Schultheis 19-94
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Tamaricaceae; Tamarix.

[ (bases 1 to 258)
Schultheis, L.M. and Baldwin, B.G.
Molecular phylogenetics of Fouquieriaceae; evidence from nuclear IDNA ITS studies.
              Wiley, E.O., Johnson, G.D. and Dimmick, W.W.
Direct Submission
Submitted (12-MAY-1999) Natural History Museum, University of
Kansas, Lawrence, KS 66045, USA
                                                                                                                                                                                                                                                                                                                                                    Gaps
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Tamarix sp. Schultheis 19-94 internal transcribed spacer 1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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/db_xref-"taxon:98320"
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100.0%; Pred. No. 5.1e+03;
tive 0; Mismatches 0;
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                                                                                                                                    /specimen_voucher="KU 22982"
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                                                                                                                                                                                                             /product="28s ribosomal RNA"
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                                                                                                                  1. .218
/organism="Mastacembelus
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2 (bases 1 to 258)
Schultheis, L.M. and Baldwin, B.G.
                                                                                               Location/Qualifiers
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2 (bases 1 to 218)
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Mastacembelus sp. 28s ribosomal RNA gene, partial sequence.
AFISO652
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Paracanthopterygii; Ophidiiformes; Ophidiidae;
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1 (bases 1 to 218)
Wiley, E.O., David Johnson, G. and Wheaton Dimmick, W. The interrelationships of Acanthomorph fishes: A total evidence approach using molecular and morphological data
Biochemical systematics and ecology. 28 (4), 319-350 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                (dases 1 to 218)
Wiley, E.O., David Johnson, G. and Wheaton Dimmick, W.
The interrelationships of Acanthomorph fishes: A total evidence approach using molecular and morphological data
Biochemical systematics and ecology. 28 (4), 319-350 (2000)
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Wiley, E.O., Johnson, G.D. and Dimmick, W.W.
Direct Submission
Submitted (12-MAY-1999) Natural History Museum, University of
                                                                                                                                                                                                                          AF150645 218 bp DNA linear VRT 22-AU
Petrotyx sanguineus 28S ribosomal RNA gene, partial sequence.
AF150645
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                  100.0%; Score 12; DB 6; I 100.0%; Pred. No. 7.9e+03;
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/specimen_voucher="KU 22948"
/db_xref="taxon:94932"
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Alee arborescens
JP 1997107975-A/4
19-07107975-B/4
19-07-1995 JP 1995294986
SHIMADA HIROAKI, OKAMOTO TOMOKO, HONDA HIDEO, FUJIMURA TATSUTO
CIZN15/09, A01H5/00, C07H21/04, C12N1/21, C12N5/10, C12N9/88, PC
                           E12962 450 bp DNA linear PAT 24-JUN-1998 CDNA encoding fragment of phosphoenolpyruvate carboxylase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type='green leaf'
1. .450
/product='Phosphoenolpyruvate carboxylase from
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H.sapiens chromosome 22 CpG island DNA genomic Msel fragment, clone
379832
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Clark, V.H., Cross, S.H., Simmen, M.W., Langford, C., Carter, N., Bickmore, W. and Bird, A.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (02-SEP-1996) ICMB, University of Edinburgh, King's
Buildings, Mayfield Rd, Edinburgh EH9 3JR, UK. E-mail contact:
VCLARR@SIVO.bio.ed.ac.uk
(bases 1 to 453)
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Shimada, H., Okamoto, T., Honda, H. and Fujimura, T..
BEC-ASE GENE OF MONCCOTYLEDON CAM PLANT
Patent: JP 199710795-A 4 28-APR-1997;
MITSUI TOATSU CHEM INC
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    .450
    /organism='Aloe arborescens'

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/organism="unidentified"
/db_xref="taxon:32644"
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Location/Qualifiers
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Chromosome 22; CpG island.
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JP 1997107975-A/4.
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/db_xref="taxon:10090"
/clone="J0521C08"
/clone_lib="Mouse eight-cell stage embryo cDNA library (M.
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                                                                               Mus musculus Sukaryota, Chordata, Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 442)
Bergstrom, D. E., Gagnon, L. H. and Eicher, E. M. Genetic and physical mapping of the dreher locus on mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                            for 30 seconds for 15 seconds for 30 seconds for 30 seconds for 30 seconds for 10 minutes
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musculus STS cDNA clone J0521C08 3', sequence tagged site.
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                                                                                                                                                                                                                                                              Contact: Eva M. Eicher
The Eicher Laboratory
The Jackson Laboratory
OOM Main Street, Bar Harbor, ME 04609 USA
Tel: 207/288-6077
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each 200 uM
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50 mM
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8.3
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                                                                                                                                                                                                                                                                                                                                                           Email: eme@jax.org
Primer A: GCACCTAGGGTAATCAAGGC
Primer B: ACCTGAGGTGATGTTTGGCT
STS size: 200
PCR Profile:
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Cross,S.H., Charlton,J.A., Nan,X. and Bird,A.P. Purification of CpG islands using a methylated DNA binding column Nat. Genet. 6 (3), 236-244 (1994) 94282070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-SEP-1996) ICMB, University of Edinburgh, King's Buildings, Mayfield Rd, Edinburgh EH9 3JR, UK. E-mail contact:
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Clark,V.H., Cross,S.H., Simmen,M.W., Langford,C., Carter,N.,
Bickmore,W. and Bird,A.P.
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/clone_lib="CGI22.1"
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/clone="301f5"
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Chromosome 22; CpG island.
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Matches 12; Conservative
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Takeshita, H., Sato, M., Shiwaku, H.O., Semba, S., Sakurada, A., Hoshi, M., Hayashi, Y., Tagawa, Y., Ayabe, H. and Horli, A. Expression of the DMBT1 gene is frequently suppressed in human lung
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PAT 17-DEC-2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (06-DEC-1998) Akira Horii, Tohoku University School of Medicine, Department of Molecular Pathology; 2-1 Seiryo-machi, Abba-ku, Sendai, Miyagi 980-8875, Japan (E-mail:horiidmail.cc.tohoku.ac.jp, Tel:81-22-717-8042, Fax:81-22-717-8047)
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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    DNA
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Patent: US 6312922-A 147 06-NOV-2001;
Location/Qualifiers
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Sequence 147 from patent US 6312922.
AR177408
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/gene="DMBT1"
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Strain was digested with AluI, Cac8I, HaeIII, NlaVI, or RsaI. Fragments in the range of 250-500 bp were gel purified and a BsYXI linker was added. The fragments were cloned into a modified Ml3mpl9 vector and transformed into E. Coli DH5alpha. Microsatelllite sequences were sorrened with labeled d(CA)15 and d(GT)15 oligonucleotide probes."
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Diversity of novel green non-sulfur bacteria from Yellowstone Unpublished
2 (bases 1 to 680)
Boomer, S.M., Dutton, B.E. and Lodge, D.P.
Direct Submission
Submitted (13-NOV-2000) Dept. of Biology, Western Oregon University, 345 Monmouth, Ave., Monmouth, OR 97361, USA
                                                                                                                                                                                                                                                                                           Gaps
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Uncultured bacterium rcr_15 16S ribosomal RNA gene, partial
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M36196 J05611
M36196.1 GI:338619
intrinsic membrane protein; synaptic vesicle protein 2A; synaptobrevin 1.
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/clone="rcr_15"
/country="USA: Rabbit Creek, Yellowstone"
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176 c 192 g 118 t
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                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

( pases 1 to 598)
Shimoda, N., Knapik, E.W., Ziniti, J., Sim, C., Yamada, E., Kaplan, S., Jackson, D., de Sauvage, F., Jacob, H. and Fishman, M.C.
Zebrafish genetic map with 2000 microsatellite markers
Genomics 58 (3), 219-232 (1999)
                                                                                                                                                                                                                    G39052 598 bp DNA linear STS 01-FEB-200 211764 Zebrafish AB Danio rerio STS genomic, sequence tagged site. G39052
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/dev_stage="Adult"
/lab_host="DH5alphaF'IQ"
/note="Vector: ml3MpH9 with added BstXI site; V-type:
Phage; Genomic DNA from a single adult Zebrafish of AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cardiovascular Research Center
Massachusetts General Hospital
Mail code 1494100A, 149 13th Street, Charlestown, MA 02129, USA
Fax: 6177265806
Email: fishman@mgh.cvrc.harvard.edu
                                                              Gaps
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                         100.0%; Score 12; DB 9; Length 498; 100.0%; Pred. No. 4.7e+03;
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94 degrees C for 1.0 minute
58 degrees C for 1.0 minute
72 degrees C for 1.5 minute
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each 375 nM
each 200 uM
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10 ul
                                                             0; Mismatches
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Primer A: GCGACCCTTTGTGATGTTT
Primer B: CATCTGATTGCTTTGTCCA
STS size: 297
PCR Profile:
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/db_xref="taxon:7955"
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SOURCE

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Cosmid end sequences from generated from flow-sorted chromosome 4 (Human Genome Center, Los Alamos National Laboratory), sequenced at the Stanford Human Genome Center.
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               Template: 25 ng
Primer: each 1 uM
dNTPE: each 200 uM
AmpliTaq Gold Polymerase: 0.07 units/ul
Total Vol: 5 ul
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Best Local Similarity 100.0%; Pred. No. 4.4e+03;
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Sequence 11 from Patent W09811228.
A70150
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/db_xref="taxon:32644"
/clone="U-U55"
                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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220. .242
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Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 761)
                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 727) Azcher, B.T. III, Ozcelik,T., Jahn,R., Francke,U. and Sudhof,T.C. Structures and chromosomal localizations of two human genes
                                                                                                                                                                                    Draft entry and computer-readable sequence for [J. Biol. Chem. (1990) in press | kindly submitted by T.C.Sudhof, 06-JUL-1990.

Location/Qualifiers
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60 degrees C for 30 seconds
72 degrees C for 23 seconds
30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 12; DB 9; Length 727; 100.0%; Pred. No. 4.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                              /note="synaptobrevin 1 (SYB1); G00-125-292"
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                                                                                                                             encoding synaptobrevins 1 and 2
J. Biol. Chem. 265 (28), 17267-17273 (1990)
91009161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="synaptobrevin 1 intron A"
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Primer B: ATGTTCTGCTTGGTTCCTCTGAC
                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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Human DNA, clone pcVP18-[1,5].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Richard M. Myers
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Polymerization:
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Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                          /gene="SYB1"
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Fax: 4157259689
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                     Homo sapiens
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                 ORGANISM
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                                                                                            AUTHORS
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                                                                          REFERENCE
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                                                                                                               TITLE
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SOURCE

Page 7

Job time: 17557 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on:

July 31, 2002, 12:21:09; Search time 165.21 Seconds (without alignments) 38.657 Million cell updates/sec

US-09-899-718A-5 26

1 cccgtctaggcgttcggtgtccggcc 26 Perfect score: Sequence:

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters:

383533 seqs, 122816752 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Issued_Patents_NA:* Database :

/cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMADIES

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Result No.	t . Score	Query Match	Query Match Length DB	DB	ID	Description
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•	2 18.6	71.5	13613	4	US-09-105-537-3	m
U	3 16.6	63.8	3061	П	US-09-570-842-1	` -
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v	5 16.6	63.8	15664	-	US-08-402-282-3	ì
υ	16.6	63.8	15664	-	US-08-508-004-3	, a
υ	7 16.6	63.8	15664	-	115-08-402-065-3	, (
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i	16.1		4411600	* -	US-09-103-640A-2	7
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٦,	9T 7	61.5	624	-	US-07-661-610C-14	14
	-	61.5	1008	4	US-09-199-637A-148	•
c 14	16	61.5	1392	4	US-08-957-351-1	Sequence 1, Appli
15	-	61.5	2101	~	US-08-637-763B-5	
ĭ	7	61.5	2101	3	US-09-170-354-5	<u>ئ</u>
c 1,	7 16	61.5	5437	m	US-07-661-610C-1	· -
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	7	61.5	80161	m	US-09-036-987A-1	ì -
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	15.		68750	7	-09-567	7
C 72	15.		68750	7	US-09-568-480-1	<u> </u>
0	-	60.8	68750	4	-60-	7
c 5,	-	8.09	68750	4	US-09-568-472-1	<u>,</u>

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22 22 22 22 24 56 66 66 66 66	1, 57,
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US-09-443-501A-2 US-09-232-200-28 US-09-232-201-28 US-08-765-907A-14 US-09-232-201-46 US-09-232-201-46 US-09-232-201-46 US-09-232-201-24 US-09-232-201-24 US-09-232-201-24 US-09-232-201-24 US-09-232-201-24 US-08-765-907A-6 US-08-765-907A-6 US-08-765-907A-6 US-08-765-907A-6 US-08-765-907A-6 US-08-765-907A-6 US-08-765-907A-6 US-08-765-907A-6 US-08-765-907A-6 US-08-765-907A-6 US-08-765-607A-6 US-08-765-607A-6 US-08-765-607A-6	US-07-639-330E-1 US-09-248-335-57
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ALIGNMENTS

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                                                              GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin; FILE REFERENCE: 600.438USI; CURRENT APPLICATION NUMBER: US/09/105,537A; CURRENT FILING DATE: 1998-06-26; NUMBER OF SEQ ID NOS: 43; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 71.5%; Score 18.6; D Best Local Similarity 84.0%; Pred. No. 5; Matches 21; Conservative 0; Mismatches
                          Sequence 7, Application US/09105537A Patent No. 6265202
                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-105-537-7
US-09-105-537-7/c
                                                                                                                                                                                                                                                                                                                                                    1248
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APPLICANT: Sherman, D.H.
APPLICANT: Sherman, D.H.
APPLICANT: Sherman, D.H.
APPLICANT: Stue, Y.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFREENCE: 600.4380S1
CURRENT APPLICATION NUMBER: US/09/105,537A
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 13613 ; Sequence 3, Application US/09105537A; Patent No. 6265202; GENERAL INFORMATION: TYPE: DNA ORGANISM: Streptomyces venezuelae RESULT 2 US-09-105-537-3

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Gaps
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LOCATION: 451..747
OTHER INFORMATION: /function= "potential open reading
                                                                                                                                                                                                                                                                                                                                                 Indels
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LOCATION: 222.425
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Beyer Jr., Wayne F. TITLE OF INVENTION: MYCOBACTERIOPHAGE SPECIFIC FOR THE ITILE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard J. Rodrick, Becton Dickinson and ADDRESSEE: Company STREET: 1 Becton Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                               Pred. No. 41;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/402,282
                      REFERENCE/DOCKET NUMBER: MOBT:024 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                       748 CATCTAGGCTTTGGGTGGCCGGC 726
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; Patent No. 5476768
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ATTORNEY/AGENT INFORMATION:
NAME: FUGIL, Donna R.
REGISTRATION NUMBER: 32,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dickson, Julie A.
Hamilton, Paul T.
Little, Michael C.
REGISTRATION NUMBER: 29,775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Pearson, Robert E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                    TELEFAX: 713/789-2679
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15664 base pairs
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                                                                    713/787-1400
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                                                                                                                                                                                                                                                                                                                               Best Local Similarity 82.69
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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EDNESS: double
                                                    TELEPHONE: 713//c.
TELEPHONE: 713/789-2679
                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Franklin Lakes
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                                                                                                                                                                                                                        TOPOLOGY: linear
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US-08-402-282-3/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                             US-08-700-576-1
                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kruger, Niels
APPLICANT: Kruger, Niels
APPLICANT: Steinbuchel, Alexander
TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE PRODUCTION OF POLYHYDROXYALKANOATES
TITLE OF INVENTION: DNA SEQUENCE USEFUL. FOR THE PRODUCTION OF POLYHYDROXYALKANOATES
FILE REFERENCE: 11899.0024. REUSOO MOBT204-1
CURRENT APPLICATION NUMBER: US/09/570,842
PRIOR FILING DATE: 1998-05-12
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                                                                  71.5%; Score 18.6; DB 4; Length 13613; 84.0%; Pred. No. 5.5; tive 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.8%; Score 16.6; DB 1; Length 3061; 82.6%; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kruger, Niels
APPLICANT: Steinbuchel, Alexander
TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE PRODUCTION
TITLE OF INVENTION: OF POLY-3-HYDROXYALKANOATES
CORRESPONDENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                      Db 11816 cgcggcgaggcgttcggtgtgcggc 11840
                                                                                                                                                             1 eccgtctaggcgttcggtgtccggc 25
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                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09570842
Patent No. RE37543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: pseudomonas putida
US-09-570-842-1
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                                                                                             Best Local Similarity 84.09
Matches 21; Conservative
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MEDIUM TYPE: Floppy
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-700-576-1/c
                                                                                                                                                                                                                                                                                        US-09-570-842-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 3061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
             US-09-105-537-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                             Query Match
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NAME/KEY: misc_feature
LOCATION: 747..1109
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 1109..2014
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 2034..2747
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 2747..3109
COTHER INFORMATION: frame" potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 3109..344
OCHER INPORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 3444..3728
THER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 3731..4855
OTHER INFORWATION: /function= "potential open reading
OTHER INFORWATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 5382..5747
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 5837..6307
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 7770..8006
OCHER INFORMATION: function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 8033..8236
OCHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 8244..9443
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 4603..7770
OTHER INFORMATION: frame" potential open reading
OTHER INFORMATION: frame"
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NAME/KEY: misc_feature
LOCATION: 4835..5376
OTHER INFORMATION: /function= "potential coding
OTHER INFORMATION: sequence"
OTHER INFORMATION: /product= "L5 gp37 homolog"
OTHER INFORMATION: frame"
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NAME/KRY: misc.feature

OTHER INFORMATION: (Inforcion "potential open reading
PROTONS 1950.1034

PROTONS 10371.1036

OTHER INFORMATION: (Inforcion "potential open reading
PRATONS 10371.1031

OTHER INFORMATION: (Inforcion "potential open reading
PRATONS 10371.1031

OTHER INFORMATION: (Inforcion "potential open reading
OTHER INFORMATION: (Inforcion "potential open reading
PRATONS 10371.10314

OTHER INFORMATION: (Inforcion "potential open reading
OTHER INFORMATION: (Inforcion "potential open reading
PRATONS 10371.10314

OTHER INFORMATION: (Inforcion "potential open reading
PRATONS 10371.10314

OTHER INFORMATION: (Inforcion "potential open reading
PRATONS 10314.1035

OTHER INFORMATION: (Inforcion "potential open reading
OTHER INFORMATION: (Inforcion "potential open reading
PRATONS 10314.1035

OTHER INFORMATION: (Inforcion "potential open reading
OTHER INFORMATION: (Inforcion "p
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LOCATION:
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LOCATION: 3731.4855
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 2034..277
VETER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 2747..3109
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 344..378.
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 411.747
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 1109..2014
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 3109.344
OCHER INFORMATION: 7function= "potential open reading
OTHER INFORMATION: frame"
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508,004
FILING DATE: 27-JUL-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/402,282
FILING DATE: 10-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                 NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-3283
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 15664 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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LOCATION: 747..1109
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NAME/KEY: misc_feature; LOCATION: 15429..15664; CTHER INFORMATION: /function= "potential open reading; OTHER INFORMATION: frame"
US-08-508-004-3
                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 5837..6307
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 8244..944..940
CHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 9450...10244
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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COCATION: 10371...10586

COCHER INFORMATION: /function= "potential open reading

OTHER INFORMATION: frame"
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LOCATION: 11115.11786
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 11917..12741
LOCHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 12748..14499
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 1471..15154
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
NAME/KEY: misc_feature
LOCATION: 5382..574
OUTER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 7770..806
LOCATION: /770..800
LOCATER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
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                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature LOCATION: 6403..7770
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TOCATION: 8033..8236
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NAME/KEY: misc_feature
LOCATION: 3109.3444
O'HER INFORMATION: /function= "potential open reading
O'THER INFORMATION: frame"
NAME/KEY: misc_feature
LOCATION: 3444.3728
O'THER INFORMATION: /function= "potential open reading
O'THER INFORMATION: frame"
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LOCATION: 8033..8236
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 11115..11786
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                          NAME/KEY: misc_feature
LOCATION: 2747..3109
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: 3731..4855
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 5382..574
OCHER INFORMATION: frame" "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 7770..8006
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 8244..9443
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 9450..10244
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
  OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 5837..6307
CHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 6403...770
OCHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 10371..10586
OCHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 4855..5376
OTHER INFORMATION: /function= "potential coding
OTHER INFORMATION: sequence"
OTHER INFORMATION: /product= "L5 gp37 homolog"
FEATURE:
                                                       ö
                                                       Gaps
                                                     ö
63.8%; Score 16.6; DB 1; Length 15664;
82.6%; Pred. No. 44;
tive 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                           US-08-402-066-3/C

Sequence 3, Application US/08402066

Sequence 3, Application US/08402066

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pactson, Julie A.
APPLICANT: Bickson, Julie A.
APPLICANT: Hamilton, Paul T.
APPLICANT: Little, Michael C.
APPLICANT: Little, Michael C.
APPLICANT: MYCOBACTERIOPHAGE SPECIFIC FOR THE TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS COMPLEX NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: 222..425
OCHER INPORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 1109..2014
OCHER INFORMATION: function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 451..747
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 747..1109
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Richard J. Rodrick, Becton Dickinson and ADDRESSEE: Company STREET: 1 Becton Drive CITY: Franklin Lakes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/402,066
                                                                                                  ATTORNEY/AGENT INPORMATION:
NAME: FUGIL, Donna R.
REGISTRATION NUMBER: 32,135
REFRENCE/DOCKET NUMBER: P-32E
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 15664 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 2034..2747
                       Best Local Similarity 82.6
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 436
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ZIP: 07417
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  Query Match
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LOCATION: 3731..4855
OTHER INFORMATION: \( \frac{7}{4}\) function= \( \text{"potential open reading oTHER INFORMATION: frame\) \( \text{Trame} \)
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                                                                                                                                                                               LOCATION: 222.7455
OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 451..747
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 747..110
CTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 3444..3728
OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
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                                                                                                       MOLECULE TYPE: DNA (genomic)
LENGTH: 15664 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature LOCATION: 1109..2014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature LOCATION: 3444..3728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature LOCATION: 3731..4855
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LOCATION: 4855..5376
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LOCATION: 5837..6307
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                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 222..425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 15429..15664
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                               NAME/KEY: misc_feature
LCGATION: 11917..12741
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                    LOCATION: 12748..14499
OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 14771..15154
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 15154.15426
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Pearson, Robert E.
APPLICANT: Dickson, Julie A.
APPLICANT: Hamilton, Paul T.
APPLICANT: Little, Michael C.
TITLE OF INVENTION: MYCOBACTERIOPHAGE SPECIFIC FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Richard J. Rodrick, Becton Dickinson and ADDRESSEE: Company STREET: 1 Becton Drive CITY: Franklin Lakes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/402,068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 11139 CGTCCAGGATTTCGGTGTCCGTC 11117
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ATTORNEY/AGENT INFORMATION:
NAME: FUGIL, DONNA R.
REGISTRATION NUMBER: 32,135
REPERRACE/POCKET NUMBER: P-321
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08402068
Patent No. 5633159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 egictaggegiteggigteegge 25
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                                                                                                                                                            NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07417
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FEATURE:

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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, Oldire M.
APPLICANT: VENTER, Oldire M.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-22007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 63.8%; Score 16.6; DB 2; Length 43280; Best Local Similarity 82.6%; Pred. No. 46; Matches 19; Conservative 0; Mismatches 4; Indels 0;
APPLICANT: SULTON, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
STREET: HOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCILLEA.
SOFTWARE: ASCILLOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: FEDLUARY 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGER CHARACTERISTICS:
LENGER DASS PAIRS
TYPE: NUCLEIC acid
STRAMBEDENES: single
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US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 cgtctaggcgttcggtgtccggc 25
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                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
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14351..19945
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20010..31199
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36249..41774
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flore
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31232..36067
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816..14234
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SOFTWARE: ASCI(DO
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LOCATION:
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; LOCATION:
US-08-804-227C-1
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FEATURE:
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; OTHER INFORMATION: /function= "potential open reading;
; OTHER INFORMATION: frame"
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NAME/KEY: misc_feature
LOCATION: 10371..10586
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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NAME/KEY: misc_feature
LOCATION: 11115..11786
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 15154..15426
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 8244..943
OCHER INPORMATION: function= "potential open reading
OTHER INFORMATION: frame"
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NAME/KEY: misc_feature
LOCATION: 12748..14498.
OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
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LOCATION: 14771..15154
OCHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                        OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
                                                                                            NAME/KEY: misc_feature
LOCATION: 8033..8236
COTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 9450..10244
OTHER INFORMATION: function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 11917...12741
OCHER INFORMATION: function= "potential open reading
OTHER INFORMATION: frame"
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Patent No. 5876991
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APPLICANT: DeHoff, Bradley S.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
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US-08-804-227C-1/c
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COMPUTER READABLE FORM:
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Best Local Similarity
Matches 19; Conserv
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US-09-199-637A-148/c
                      MEDIUM TYPE:
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APPLICANT:
APPLICANT:
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                                                                                                                                                   OTHER INFORMATION: CDC 1551
COTHER INFORMATION: "n" bases at various positions throughout the sequence COTHER INFORMATION: represent a, t, c or g
92-09-103-8408-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WINTER, Oohn C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 2456-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
UNMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                              0; Gaps
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                                                                                                                                                                                                                                                                                 Query Match 63.1%; Score 16.4; DB 4; Length 4403765; Best Local Similarity 76.9%; Pred. No. 40; Matches 20; Conservative 0; Mismatches 6; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/07661610C
Patent No. 5292643
GENERAL INFORMATION:
APPLICANT: Shibano, Yuji
APPLICANT: Toyoda, Hideyoshi
APPLICANT: Obtan, Raulaki
TITLE OF INVENTION: Fluaric Acid Resistant Genes
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 497133 ccggtcttgcggctcggtgtccgggc 497158
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OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                          ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                            1 cccgtctaggcgttcggtgtccggcc 26
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Best Local Similarity 76.9%
Matches 20; Conservative
                      PatentIn Ver. 2.1
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                    SEQ ID NO 2
LENGTH: 4403765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-661-610C-14/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-103-840A-1
                                                                                     TYPE: DNA
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                        SOFTWARE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: TSONGALIS, JOHN
TITLE OF INVENTION: VIRQUENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REPRENCE: 00786/361002
CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1999-11-25
PRIOR FILING DATE: 1999-11-25
             COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16; DB 4;
Pred. No. 73;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 72;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 437
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16;
                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 529264 aman F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2292-010-0
                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/661,610C
FILING DATE: 19910228
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 148, Application US/09199637A; Patent No. 6355411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mahajan-Miklos, Shalina
Tan, Man-Wah
Cao, Hui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 CATCGAAACGTTCGGCGTCCGGCC 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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TELEPHONE: (703)521-4500
TELEFAX: (703)466-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 cgtctaggcgttcggtgtccggcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.5%;
79.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick
APPLICANT: Goodman, Howard M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rahme, Laurence G.
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drenkard, Eliana
                                                                                                                                                                                                                                                                                                                                       LENGTH: 624 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 79.2
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: unknown
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; NAME/KEY:
; LOCATION:
US-08-637-763B-5
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                Sequence 1, Application US/08957351

Patent No. 6306586

GENERAL INFORMATION:
APPLICANT: Semina, Elena
APPLICANT: Murray, Jeffrey C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CATARACTS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 61.5%; Score 16; DB 4; Length 1392; Best Local Similarity 79.2%; Pred. No. 74; Matches 19; Conservative 0; Mismatches 5; Indels
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COUNTRY: USA
ZIP: 20006-1812
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
OFFWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08637763B
Patent No. 5849559
GENERAL INCORMATION:
APPLICANT: VAN DER WOUW, Monique J.A. et al
TITLE OF INVENTION: ARABINOXYLAN DEGRADING ENZYME
CORRESPONDENCE: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READALLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: InP PC compatible
COMPUTER: InP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,351
FILIG DATE: 24-OCT-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: ATTORNEY AGENT
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-024.01
TELEDOMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEPAX: 617-832-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 1119 CCAGTCTAGGCGACCCTGTCCGG 1096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1392 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: CDNAUS-08-957-351-1
                                                                                                                                                                                                                                                                                                                                          02109-2170
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US-08-957-351-1/c
                                                                                                                                                                                                                                                                       CITY: BOS
STATE: MA
COUNTRY:
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OTHER INFORMATION: /product= "arabinoxylan degrading OTHER INFORMATION: enzyme" OTHER INFORMATION: /gene= "axda" OTHER INFORMATION: /standard_name= "arabinoxylan degrading enzyme" FEATURE:
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0
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,763B
FILING DATE: 15-AUG-1996
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: MATASHIGE, Kate H.
REGISTRATION NUMBER: 4615-0066.00
TELECOMMUNICATION INFORMATION:
TELEFONE: (202) 887-1500
TELEFAX: (202) 887-1500
TELEFAX: (202) 887-0763
TELERATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 2101 base pairs
TYPE: nucleic acid
STRANDEDMESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: July 31, 2002, 12:23:47 Job time: 11850 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266 CACGTCTAGACTTTCGATGCCCGG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 cccgtctaggcgttcggtgtccgg 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Aspergillus niger
STRAIN: CBS 120.49
                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 79.23
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sig_peptide
784..861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mat_peptide
862..1779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: TATA_signal LOCATION: 665..670
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784..1779
                                                                                                                                                                                                                                                                                                                                                                                        NO
                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
FEATURE:
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

July 31, 2002, 12:12:01; Search time 5855.71 Seconds (without alignments) 59:928 Million cell updates/sec Run on:

US-09-899-718A-5 26 1 cccgtctaggcgttcggtgtccggcc 26

Title: Perfect score:

Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

13736207 seqs, 6748477542 residues Searched:

27472414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

EST: *

gb_gss:*
em_gss_hum:*
em_gss_inv:*
em_gss_pln:*
em_gss_vrt:* 1: em_estba:*
2: em_esthum:*
3: em_esthu:*
4: em_esthu:*
5: em_estpu:*
7: em_estpu:*
7: em_estpu:*
1: gb_est1:*
10: gb_est2:* 9: 110: 111: 112: 115:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	BH506552 BOGFR94TF BH428H42 BOGSZ83TR BH321002 AG-ND-180 BM072919 MEST55-H0 BF770774 RC1-IT001 AL208H41 TETFACHON A2496643 1M033K08 BM398961 5009-0-51 BE748192 601571585 AGO60278 Pan troog1 BE869446 601446101 AW949909 EST361979 BE818796 602779143 BE462300 EST341545 BI490136 603739172 BI490136 603739172 BI490136 603739172 BI925736 EST345652 BF867684 963033905	
SUMMARIES	BH506552 BH428842 BH428842 BH3291002 BM072919 BF770774 CNS02PLG AZ496643 BM398961 BE748192 AG060278 BE869446 BE869446 BE8182909 BE818796 BE462300 B1490136 B1925736	
DB	44444444444444444444444444444444444444	
% Query Match Length DB	668 747 420 700 701 711 319 745 845 631 633 633 649 702 702 702	
% Query Match	73.8 711.5 711.5 70.0 69.2 69.2 69.2 69.2 67.7 67.7 67.7 67.7	
Score	19.2 19.2 18.6 18.6 18.7 18.7 19.8 10.7 10.6 10.7 10.6 10.7 10.6 10.7 10.7 10.7 10.7 10.7 10.7 10.7 10.7	
Result No.	11 28 38 47 11 11 11 11 11 11 11 11 11 11	
' Re	0 000 00 0	

668 bp DNA linear GSS 13-DEC-2001 Brassica oleracea genomic clone BOGFR94, DNA	BOGF	BH506552 BOGFR94TF	TION	LOCUS
			1 1	RESULT BH506552
ALIGNMENTS				
10 BG281333 BG281333	84	.2 66.	П	4
519 60190303	8.1			C 44
10 BE727948 BE727	7.	.2 66.		4
10 BG747901 BG747901 60270575	, ,	.2 66.	-	4 -
10 BG419972 BG419972	39	.2 66.	Π,	4
10 BG983477 BG983477	99	.2 66.	1	39
10 EG902903 BG902903 9 AI398765 A	9	.2 66.	+ ~	38
10 BG992087 BG99208	90	.2 66.		36
10 BI774972 BI774972	S	.2 66.	П	m ·
9 BE161996	5,	.2 66.	П	n
9 AI222008 AI22200	4	.2 66.	Н	m
38 10 H15755 H15755	4	.2 66.	1 ~	m
76 IO N60925	ν, «	. 2 00.	٦,	0 0 1 1
55 10 BE937624 BE937624	3	.2 66.	Τ,	~
48 10 BE937659 BE937659 MR1-TN00	37	.2 66.	1	28
18 10 BE937644 BE937644	36	.2 66.	1	27
23 IO BESSIE// BESSIE/ 14 9 ATJ33850	, w	. 2		26.
15 10 BF770115 BF770115 RCI-ITO	, ,	.2 66.	٦,	24
47 10 BI834829 60309028	117	.6 67.	7	7
32 10 BF180488 BF180488	9	.6 67.	٦	N
11 10 BI601214 60324572	6	.6 67.	Н	C)
77 10 BI462741 BI462741 60320219	80	.6 67.	1	C)
57 10 BF241175 BF241175	ö	.6 67.	7	c 19
01 10 ppg02840	à	6	-	-

RESULT 1 BH506552	
rocus	dq 899
DEFINITION	BOGFR94TF BOGF Brassica oleracea genomic clone BOGFR94, DNA
ACCESSION	Sequence: BH506552
VERSION	BH506552.1 GI:17714649
SOURCE	Brassica oleracea
ORGANISM	Brassica oleracea
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
	Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE	1 (bases 1 to 668)
AUTHORS	Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
TITLE	Whole genome shotgun sequencing of Brassica oleracea
JOURNAL	Unpublished (2001)
COMMENT	Other_GSSs: BOGFR94TR
	Contact: Chris Town
	TIGR
	9712 Medical Center Drive, Rockville, MD 20850, USA.
	Tel: 301-838-3523
	Fax: 301-838-0208
	Email: cdtown@tigr.ord ,
	DNA is from a doubled haploid provided by Tom Osborn.
	Seq primer: TF
	Class: sheared ends.
FEATURES	Location/Qualifiers
source	1668
	/ordanism="Brassica oleracea"
	/strain="TO1000DH3"
	/db_xref="taxon:3712"
	/clone="BOGFR94"
	/clone_lib="BOGF"
	/note="Vector: pHOS1: Site 1: Bstxr: 2-3 kb sheared
	genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT	195 a 140 c 125 g 208 t
ONTOTIO	

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Direct Submission of BAC-end sequences from Anopheles gambiae
                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: schnable@iastate.edu
                   Unpublished (2001)
Other_GSSs: AG-ND-180A21.TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 CCCTTCTGGCCGTGCGGTGTCCGGC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 cccgtctaggcgttcggtgtccggc 25
                                                         Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BM072919.1 GI:16916614
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="PEST
                                                                                                                                                                                                                                                                                                                                               partial digest.
Seq primer: M13 Rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      .420
                                                                                                                                                                                                                                                                                                                                                                                 Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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   TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BM072919
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                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
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                                         COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 420)
Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AG-ND-180A21.TR ND-TAM Anopheles gambiae genomic clone AG-ND-180A21
                                                                                                                                                                                                                 GSS 12-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic DNA inserted into pHOS1 using BstXI linkers" 150 c 128 g 265 t
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                                                                                                                                                                                                                     BH428842 747 bp DNA linear GSS 12-1
BOGSZ83TR BOGS Brassica oleracea genomic clone BOGSZ83, DNA
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 73.8%; Score 19.2; DB 12; Length 747; Best Local Similarity 87.5%; Pred. No. 3.9e+02; Matches 21; Conservative 0; Mismatches 3; Indels 0;
   73.8%; Score 19.2; DB 12; Length 668; 87.5%; Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA is from a doubled haploid provided by Tom Osborn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                              own, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9712 Medical Center Drive, Rockville, MD 20850, USA.
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                                                                                                                      534 CAGTCTTCGCGTTCGGTGTCCGGC 557
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                                                                                2 ccgtctaggcgttcggtgtccggc 25
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BH428842.1 GI:17614563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cdtown@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Other_GSSs: BOGSZ83TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Chris Town
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                                               21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                       Brassica oleracea
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           Query Match
Best Local Similarity
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(<http://depts.washington.edu/ventures/collabtr/direct/index.htm>#b
rt). Overall sequence quality assessment and vector trimming were
conducted using the Lucy software (<http://www.tigr.org/softlab/>).
Lucy parameters were set to ensure an overall trimmed quality of
97.5% or better without any vector fragments in the chosen
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                                                                                                                                                                                                                                                                                                                                                                                        to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&W University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                  F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae
                                                                                                                                                                                               Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Individual basecall and confidence value were assigned using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olu, F., Cui, F., Guo, L., Ashlock, D.A, Wen, T.J. and Schnable, P.S. Diu, F., Cui, F., Guo, L., Ashlock, D.A, Wen, T.J. and Schnable, P.S. Expressed Sequence Tags from B73 Maize Seedlings and Silks Unpublished (2001)
Contact: Patrick S. Schnable Schnable Laboratory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Iowa State University
QAGB Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEST55-H08.T3 ISUM4-TN Zea mays cDNA clone MEST55-H08 3', mRNA
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Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="NN-TAM"
/clone_lib="NN-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
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1 (bases 1 to 576)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Brunstein, G. H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 12-JAN-2001
                                                                                               BACKWARD: Backward PCR primer sequence, primer T3 (ATT AAC CCT CAC
                                                              FORWARD: Forward PCR primer sequence, primer T7-1 (AA TAC GAC TCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF770774 576 bp mRNA linear EST 12-JAN-200 RCL_IT0013-251100-012-e09 IT0013 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed
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0
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20202663
                                                                                                                                Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers
                                                                                                                                                                                                                                                /clone_lib="ISUM4-TN"
/tissue_type="Seedling and silk"
/lab_host="DH10B"
                                                                                                                                                                                                                 /db_xref="taxon:4577"
                                                                                                                                                                                /organism="Zea mays"
/cultivar="B73"
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Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome broject. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-IT0013-251100-012-e09&t3=2000-11-25&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Included" |
/clone_lib="Included" |
/dev_stage="Adult" |
/dev_stage="Adult" |
/dev_stage="Adult" |
/note="Organ: epid_tumor; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
Porfiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.

1142 c 206 g 119 t
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Tetraodon nigroviridis genome survey sequence T7 end of clone
15005 of library G from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostcmi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthomorpha; Terraodontidae; Tetraodontidae; Tetraodon.

[ (pases lto 771)

Roest-Crollius, H., Jaillan, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Charaterization and repeat analysis of the compact genome of the freshwater pufferish Tetraodon nigroviridis
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cost-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.0%; Score 18.2; DB 10; Length 576; 87.0%; Pred. No. 9.6e+02; Live 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                       Seq primer: puc 18 forward
High quality sequence start: 31
High quality sequence stop: 575.
Location/Qualifiers
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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us-09-899-718a-5.rst

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601571585F1 NIH_MGC_55 Homo sapiens CDNA clone IMAGE:3838557 5', mPNA secondary
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of pWD42 (gil4732114)gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
                                                                   purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
146 c 130 g 195 t
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Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel,
,J. and Klobutcher,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST from Terrahymena thermophila, strain CU428.1, growing cells Unpublished (2002)
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Hymenostomatida; Tetrahymenina; Tetrahymena
                                                                                                                                                                                                                                                              69.2%; Score 18; DB 12; Length 319; 80.8%; Pred. No. 1e+03; Live 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    920 E. 58th Street, Chicago, IL 60637, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecular Genetics and Cell Biology
University of Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: apturkew@midway.uchicago.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   745 bp
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Best Local Similarity 80.89
Matches 21; Conservative
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Fax: 773 702 3172
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BE748192
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ496643
1M0333K08F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0333K08 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain X110-Gold, T1-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                        /clone_lib="G"
/clone_lib="G"
/note="Genoscope sequence ID : COAGIS6AB03LP1-end : T7"
/ note="Genoscope sequence ID : TOAGIS6AB03LP1-end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                    70.0%; Score 18.2; DB 12; Length 771; 87.0%; Pred. No. 1e+03; tive 0; Mismatches 3; Indels 0;
                                       /organism="Tetraodon nigroviridis"
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Seq primer: CGTTGTAAAACGACGGCCAGT
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/clone="UUGC1M0333K08"
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                                                           /db_xref="taxon:99883"
/clone="156C05"
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Matches 20; Conservative
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Fax: 801 585 7177
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Direct Submission Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:sl8145-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the RsD process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 20-0CT-2000
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/clone_lib="NIH_MGC_65"
/clone_lib="NIH_MGC_65"
/tissue_type="adenocarcinoma"
/lab_host="NHH (Pape-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1425)
NIH-MGC http://mgc.nci.nih.gov/.
NaH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE869446 1425 bp mRNA linear EST 20-OCT-20 01446101F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849888 5',
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: They the Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.b column: 01
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/clone_lib="pTB Chimpanzee Male BAC Library"
227 c 400 g 262 t 39 others
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80.8%; Pred. No. 1.3e+03;
"wismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-047L15.F"
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/db_xref="taxon:9606"
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Location/Qualifiers
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Location/Qualifiers
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BE869446
BE869446.1 GI:10318222
                                                                                                                                                                                                                                                             clone tracking errors.
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/clone=lib="NIH_MGC_55"
/tissue_type="from acute myelogenous leukemia"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site_1: Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc); Double-stranded cDNR was prepared from call line RNA.
); Double-stranded cDNR was prepared from call line RNA.
5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC'3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC'3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC'3' and 3' adaptor sequence: 5'-CATGGCCATTATGGCC'3' and 3' adaptor sequence: 5'-CATGGCCATTATGGCC'ATTATGGCC'ATTATGGCC'ATTATGGCC'ATTATGGCC'ATTATGGCC'ATTATGG
                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 845)

NIH-WGC http://mgc.noi.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Ggapbs-rémail.nih.gov
Tissue Procurement: ArC

CONA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

Http://magg.llnl.gov
Plate: LLCMS.S. row: i.column: 22
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GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-047L15.F.
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Pan troglodytes DNA, clone: PTB-047L15.F, genomic survey sequence.
AG060278
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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BAC end sequences of Library PTB
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/db_xref="taxon:9606"
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Location/Qualifiers
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Best Local Similarity 80.88
Matches 21, Conservative
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l (bases 1 to 499)
van der Hoeven, R.S., Bezzeredes, J.L., Matern, A.L., Holt, I.E., Liang, F., Hansen, T., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D. Generation of ESTs from tomato flower tissue, 0-3 mm buds
Contact: CUGI
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/clone="cTOA12G14"
/clone_lib="tomato flower buds 0-3 mm, Cornell University"
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://maqg.llnl.gov
Plate: LLMM10822 row: e column: 11
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: brain; vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
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loss"
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EST324564 tomato flower buds 0-3 mm, Cornell University
Lycopersicon esculentum cDNA clone cTOA12G14, mRNA sequence.
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100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
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Pred. No. 1.7e+03;
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/cultivar="TA496"
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/clone="IMAGE:4914802"
/clone_lib="NCI_CGAP_Brn67"
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Location/Qualifiers
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83.3%;
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Best Local Similarity
Matches 20; Conserv
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            AUTHORS
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5', mRNA sequence.
BG818796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW949909 633 bp mRNA linear EST 01-JUN-2000 EST361979 MAGE resequences, MAGA Homo sapiens cDNA, mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 633)
1 (bases 1 to 633)
1 (bases 1 to 634)
1 (bases 1 to 634)
2 (bases 1 to 635)
2 (based 1 to 636)
3 (based 1 to 637)
3 (based 2 to 637)
4 (based 3 to 647)
5 (based 3 to 647)
6 (based 3 to 647)
6 (based 3 to 647)
7 (based 3 to 647)
8 (based
            Library constructed by Life
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 495)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray Unpublished (2000)

Unpublished (2000)

Unpublished (2000)

Unpublished (2000)

Unackenbush

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 3528

Fax: 301 838 0208

Email: johnq@tigr.org
                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                    Score 18; DB 10;
Pred. No. 1.4e+03;
0; Mismatches 5;
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153 g 132 t
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/db_xref="taxon:9606"
/clone_lib="WAGE resequences,
/note="Vector: pBluescriptSKm"
         Average insert size 1.8 kb.
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                                          Technologies.
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80.8%;
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                                                                562 c
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Best Local Similarity 80.8
Matches 21; Conservative
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TITLE

SOURCE

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COMMENT

ORIGIN

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//note="Organ: pooled brain, lung, testis; Vector:
//note="Organ: pooled brain, lung, testis; Vector:
pcWW-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1:8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B1490136 591 bp mRNA linear EST 28-AUG-2001 603031972F1 NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5173480 5',
                                                                                                                                                                                                                                                                                                                                                                                  ö
/tissue_type="flower"
/dev_stage="0-3mm buds"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xho1; supplier: Tanksley; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
slae-separated while remaining frozen."
132 c 128 g 127 t
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1 (bases 1 to 591)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
column: 17
High quality sequence stop: 591.
Location/Qualifiers
I..591
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:517480"
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                          67.7%; Score 17.6; DB 10; Length 499; 83.3%; Pred. No. 1.7e+03; Live 0; Mismatches 4; Indels 0
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BI490136
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BI490136/c
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Gaps

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1 cccgtctaggcgttcggtgtccgg 24

20; Conservative

Matches

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58 CCCGACGATGCGCTCGGTGTCCGG 35
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Search completed: July 31, 2002, 12:12:05 Job time: 13478 sec

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July 31, 2002, 14:11:17; Search time 720.8 Seconds (Without alignments) 61.931 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                  1736436 seqs, 858457221 residues
                                                                                                                                                                                                                                              1 cccgtctaggcgttcggtgtccggcc 26
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Maximum Match 100%
Listing first 45 summaries
                                                                              OM nucleic - nucleic search, using sw model
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26
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Perfect score:
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*** SIDSI/gcgdata/hold-geneseqn-embl/NA1980.DAT:**

\$\times \text{SIDSI/gcgdata/hold-geneseqn-embl/NA1981.DAT:*} \times \text{SIDSI/gcgdata/hold-geneseqn-embl/NA1981.DAT:*} \times \text{SIDSI/gcgdata/hold-geneseqn-embl/NA1981.DAT:*} \times \text{SIDSI/gcgdata/hold-geneseqn-embl/NA1983.DAT:*} \times \text{SIDSI/gcgdata/hold-geneseqn-embl/NA1984.DAT:*} \times \text{SIDSI/gcgdata/hold-geneseqn-embl/NA1986.DAT:*} \times \text{SIDSI/gcgdata/hold-geneseqn-embl/NA1980.DAT:*} \times \text{SIDSI/gcgdata/hold-geneseqn-embl/NA1980.DAT:*} \times \text{SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1980.DAT:*} \times \text{SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1980.DAT:*} \times \text{SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1990.DAT:*} \times \text{SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1991.DAT:*} \times \text{SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1991.DAT:*} \times \text{SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1991.DAT:*} \times \text{SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1992.DAT:*} \times \text{SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1995.DAT:*} \times \text{SIDS /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/Na1998.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/Na1099.DAT:*/SIDS1/gcgdata/hold-geneseqn/embseqn/geneseqn-emb1/Na2000.DAT:*/SIDS1/gcgdata/hold-geneseqy/geneseqn-emb1/Na2001a.DAT:*/SIDS1/gcgdata/hold-geneseqy/geneseqn-emb1/Na2001b.DAT:* /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	S. venezuelae deso	S. venezuelae deso	S. venezuelae deso	Micromonospora med	Human pentraxin I	Human breast cell	Human foetal liver	Probe #4686 for de	Human brain expres
SUMMARTES			ID	AAZ87286	AAZ87284	AAZ87319	AAF30757	AAH41415	ABA46067	ABA56605	ABA26220	AAK04749
			EB CB	21	21	21	22	22	22	22	55	22
			re Match Length DB I	1248	12441	13613	47981	1680	381	381	381	381
	dР	Query	Match	71.5	71.5	71.5	67.7	66.2	65.4	65.4	65.4	65.4
			Score	18.6	18.6	18.6	17.6	17.2	17	17	17	17
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98US-0105537. 99WO-US14398

26-JUN-1998; 25-JUN-1999;

06-JAN-2000

(MINU) UNIV MINNESOTA

Human bone marrow	Probe #4804 for ge	Probe #4913 used t	Probe #4649 used t	Polycistronic oper	Human colon cancer	Human reproductive	Human secreted pro	Nucleotide sequenc	G. oxydans autonom	Mycobacteriophage	Mycobacteriophage	Mycobacteriophage	Nhel-G/Spel fragme	Tylactone synthase	Drosophila melanog	Human secreted pro	Human nervous syst	Human nervous syst	Drosophila melanog	Drosophila melanog	Mycobacterium tube	Prepro-polygalactu	Human cDNA encodin	S	Drosophila melanog	1a	Drosophila melanog	Drosophila melanog		Mycobacterium tube	Mycobacterium tube	Human digestive sy	Human liver associ	Megalomicin polyke	Drosophila melanog
AAK30275	AAI14871	AAI36227	AAI04658	AAQ06685	AAH35021	AAL04931	AAC12097	AAV22799	AAX57803	AAT09312	AAT70492	AAT66130	AAT51224	AAT80413	ABL27597	AAF22378	ABA16862	ABA19759	ABL06699	ABL18703	AAS03788	AAQ11271	AAF93794	AAF77899	ABL07609	ABL06698	ABL18702	ABL07608	ABL09808	AAI99683	AA199682	AAK88761	AAS31795	AAF30761	ABL25667
22	22	22	22	11	22	22	21	19	20	17	18	18	18	18	23	21	22	22	23	23	22	12	22	22	23	23	23	23			7	22			
381	381	381	381	1463	2443	32249	120	3061	4599	15664	15664	15664	15664	43280	952	1175	1343	1343	1571	1959	2310	2495	2547	3090	3442	3728	4109	12713	24221	4403765	4411529	303	303	528	280
65.4	65.4	65.4	65.4	65.4	65.4	65.4	63.8	63.8	63.8	63.8	63.8	63.8	63.8	63.8	63.1	63.1	63.1	63.1	63.1	63.1	63.1	63.1	63.1	63.1	63.1	63.1	63.1	63.1	63,1	63.1	63.1	62.3	62.3	62.3	62.3
17	17	17	17	17	17	17			•		•	•		16.6	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4			16.4				16.2	16.2	•	•
10	11	12	13	14	15	16	17	18	19	20	21		23	24	25	56	27	28	58	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
ပ	υ	U	υ			Ö		υ	υ	Ö	ပ	U	O	O	Ö	O	U			Ö	U		U	υ	υ	O	υ	ပ	ပ						

ALIGNMENTS

Desosamine biosynthesis; macrolide; polyketide; methymycin; pikromycin; neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase; biopolymer; antibiotic; chemotherapeutic; immunosuppressant; asthma, chronic obstructive pulmonary disease; respiratory inflammation; hypercholesterolaemia; crop protection agent; ds. S. venezuelae desosamine biosynthetic gene desI, SEQ ID NO:7. Location/Qualifiers 1..1248 /*tag= a Streptomyces venezuelae ATCC15439 /*tag= a /product= "DesI" AAZ87286/c ID AAZ87286 standard; DNA; 1248 BP. (first entry) WO200000620-A2 05-JUN-2000 AAZ87286; RESULT Desosamine and macrolide biosynthetic gene clusters, useful for, e .g.

synthesis of methymycin and pikromycin

Sherman DH, Liu H, Xue Y, Zhao L;

WPI; 2000-160679/14.

P-PSDB; AAY77179

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98US-0105537. 99WO-US14398.

25-JUN-1999; 26-JUN-1998;

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production of biologically active macrolides. The macrolide biosynthetic production of biologically active macrolides. The macrolide biosynthetic proteins are useful for synthesis of methymycin, pikromycin, neomethymycin and narbomycin. The alternative termination of polyketide synthesis may be useful to prepare novel antibiotics and polyhydroxyalkanoate (PHA) monomers. The compounds produced by the recombinant host cells are useful as biopolymers, e.g., in packaging or biomedical applications, to engineer PHA monomer synthases or to prepare biologically active agents, such as chemotherapeutics, in packaging or immunosuppressants, agents to treat asthma, chronic obstructive pulmonary disease as well as other diseases involving respiratory inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cholesterol-lowering agents or macrolide-based antibiotics which are active against a variety of organisms, e.g., bacteria, including multi-drug resistant pneumococci and other respiratory pathogens, as well sulfing insecticides) via expression of polyketides in plants. Sequences AA287286-287294 represent desosamine biosynthetic genes from streptomyces venezuelae ATCC 15439, which encode proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Desosamine biosynthesis; macrolide; polyketide; methymycin; pikromycin;
                                                                                                                                                                                                                                                        The invention relates to an isolated and purified nucleic acid segment comprising a desosamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not derived from the eryC gene cluster of Saccharopolyspora erythraea or Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster, or fragments thereof. The macrolide biosynthetic gene cluster encodes proteins which synthesise methymycin,
                                                                                                                                        Desosamine and macrolide biosynthetic gene clusters, useful for, e .g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase; blopolymer; antibiotic; chemicherapetic; immunosuppressant; asthma, chronic obstructive pulmonary disease; respiratory inflammation; hypercholesterolaemia; crop protection agent; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S. venezuelae desosamine biosynthetic gene cluster pikB, SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    compounds. Recombinant or augmented cells comprising the desosamine and/or macrolide biosynthetic gene clusters are useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                pikromycin, neomethymycin, narbomycin or a combination of these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.5%; Score 18.6; DB 21; Length 1248; 84.0%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1248 BP; 177 A; 546 C; 377 G; 148 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                 synthesis of methymycin and pikromycin
                                                                                                                                                                                                             Claim 3; Page 353-354; 438pp; English.
                   Xue Y, Zhao L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1068 CGCGCCGAGGCGTTCGGTGCGGC 1044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ87284 standard; DNA; 12441 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 84.0 tes 21; Conservative
                 Liu H,
                                                                   WPI; 2000-160679/14.
                                                                                              P-PSDB; AAY77181
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                   Sherman DH,
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as biopolymers, e.g., in packaging or biomedical applications, to engineer PHA monomer synthases or to prepare biologically active agents, such as chemocherapeutics, immunosuppressants, agents to treat asthma, chronic obstructive pulmonary disease as well as other diseases involving respiratory inflammation, cholesterol-lowering agents or macrolide-based antibiotics which are active against a variety of organisms, e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and/or macrolide biosynthetic gene clusters are useful for the production of biologically active macrolides. The macrolide biosynthetic proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        are useful for synthesis of methymycin, pikromycin, neomethymycin and narbomycin. The alternative termination of polyketide synthesis may be useful to prepare novel antibiotics and polyhydroxyalkanoate (PHA) monomers. The compounds produced by the recombinant host cells are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comprising a desosamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not derived from the eryC gene cluster of Saccharopolyspora erythraea or Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster, or fragments thereof. The macrolide biosynthetic gene cluster encodes proteins which synthesise methymycin, parkomycin, neomethymycin, narbomycin or a combination of these compounds. Recombinant or a ungmented cells comprising the desosamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          respiratory pathogens, as well as viral parasitic pathogens, or as crop protection agents (e.g., fungicides or insecticides) via expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Desosamine biosynthesis; macrolide; polyketide; methymycin; pikromycin; neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase; biopolymer; antibiotic; chemotherapeutic; immunosuppressant; asthma, chronic obstructive pulmonary disease; respiratory inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated and purified nucleic acid segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polyketides in plants. The present sequence represents the desosamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.5%; Score 18.6; DB 21; Length 12441; 84.0%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bacteria, including multi-drug resistant pneumococci and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12441 BP; 1704 A; 4294 C; 4686 G; 1757 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 281-287; 438pp; English.
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Best Local Similarity
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88 X C C C C C C C C C C C C C C C C X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X
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/product= "PikB gene cluster protein #6 (AAY77208)"
/note= "No termination codon given in the specification"
/transl_except= (pos:8270..8272, aa:val)
/transl_except= (pos:8273..8275, aa:Thr)
/transl_except= (pos:8276..8278, aa:Gly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprising a desosamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not derived from the eryc gene cluster of Saccharopolyspora erythraea or Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster, or fragments thereof. The macrolide biosynthetic gene cluster encodes proteins which synthesise methymycin, pikromycin, neomethymycin, narbomycin or a combination of these
                                                                  'product= "PikB gene cluster protein #1 (AAY77204)"
'note= "No initiation codon given in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated and purified nucleic acid segment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "PikB gene cluster protein #10 (AAY77211)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "PikB gene cluster protein #11 (AAY77212)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "PikB gene cluster protein #9 (AAY77210)"
complement (13706..15043)
                                                                                                                            product= "PikB gene cluster protein #2 (AAY80998)"
                                                                                                                                                                                                               product= "PikB gene cluster protein #4 (AAY77206)"
/transl_except= (pos:6837..6841, aa:Gln)
7492..8205
                                                                                                                                                                                                                                                                     /product= "PikB gene cluster protein #5 (AAY77207)"
complement (7942..8205)
                                                                                                                                                                                                                                                                                                                                                                                                                               /product="PikB gene cluster protein #7 (AAY80999)"
complement (11271..12149)
                                                                                                                                                            *tag= c
product= "PikB gene cluster protein #3 (AAY77205)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "PikB gene cluster protein #8 (AAY77209)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (12342..13799)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synthesis of methymycin and pikromycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Figure 32; 438pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhao L;
            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15404..15574
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             Key
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compounds. Recombinant or augmented cells comprising the desosamine and/or macrolide biosynthetic gene clusters are useful for the production of biologically active macrolides. The macrolide biosynthetic proteins are useful for synthesis of methymycin, pikromycin, neomethymycin and narbomycin. The alternative termination of polyketide synthesis may be useful to prepare novel antibiotics and polyhydroxyalkanoate (PHA) monomers. The compounds produced by the recombinant host cells are useful as biopolymers, e.g., in packaging or biomedical applications, to engineer PHA monomer synthases or to prepare biologically active agents,
                                                                                                                                                      such as chemotherapeutics, immunosuppressants, agents to treat asthma, chronic obstructive pulmonary disease as well as other diseases involving respiratory inflammation, cholesterol-lowering agents or macrolide-based antibiotics which are active against a variety of organisms, e.g., bacteria, including multi-drug resistant pneumococci and other respiratory pathogens, as well as viral parasitic pathogens, or as crop protection agents (e.g., fungicides or insecticides) via expression of polyketides in plants. The present sequence represents the desosamine biosynthetic gene cluster (pix) from Streptomyces venezuelae ATCC 15439, as given in figure 32.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "TDP-4-keto-6-deoxyhexose 3,4-isomerase"
/note= "encodes AAB82202"
2072..3382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Micromonospora megalomicea megalomicin biosynthetic gene cluster.
                                                                                                                                                                                                                                                                                                                                                                                                      DB 21; Length 13613;
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/note= "eryCIII homologue; encodes AAB802203"
                                                                                                                                                                                                                                                                                                                                                   Sequence 13613 BP; 1858 A; 4733 C; 5092 G; 1930 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Megalomicin; meg gene; polyketide synthase; antibiotic; motilide; antiparasitic; ds.
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2,3-dehydratase"
                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
                                                                                                                                                                                                                                                                                                                                                                                                    71.5%; Score 18.6; I ilarity 84.0%; Pred. No. 31; Conservative 0; Mismatches
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/note= "encodes AAB82204'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Micromonospora megalomicea subsp. nigra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 11816 cgcggcgaggcgttcggtgtgcggc 11840
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/qene= "meqDVI"
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/gene= "megDII"
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/gene= "megY"
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hes 21; Conserva
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Matches
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    /product= "TDP-4-keto-6-deoxyhexose 4-ketoreductase"
/note= "eryVIV, dnmV homolgoue; encodes AAB82208"
complement (8228..9220)
                                                                                                                                                                                                                                                                                                      /*tag= k
/gene= "megBIV"
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//forte= "encodes AAB82211"
12181..22821
                                                                                          /*tag= g
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/product= "TDP-4-keto-6-deoxyhexose 3,5-epimerase"
//forde= "eryBVIII, dnmU homologue, encodes AAB82207"
7220..8206
                                                                                                                                                                                                      /gene= "megBII-1(megDVII)"
/groduct= "TDP-4-keto-6-deoxyhexose 2,3-reductase"
/note= "encodes AAB82209"
complement (9226..10479)
                                       /*tag= f
/gene= "megDIII"
/product= "daunosaminyl-N,N-dimethyltransferase"
/note= "eryCVI homologue; encodes AAB82206"
6592..7197
                  'note= "eryC1, DnrJ homologue, encodes AAB82205"
                                                                                                                                                                                                                                                                                                                                                                                       note= "polyketide synthase; encodes AABB2212" (2505..13470
                                                                                                                                                                                                                                                                                                                                                                          /product= "megalomicin 6-deoxyerthronolide B synthase 1"
                                                                                                                                                                                                                                                                     /product= "TDP-mycarose glycosyltransferase"
/note= "encodes AAB82210"
complement (10483..11424)
'product= "TDP-3-keto-6-deoxyhexose
           3-aminotransaminase"
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"megA"
- "ACP-1"
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/gene= "megA"
___ion= "KS1"
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/gene= "megA"
/function= "KR1"
17947..18207
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ion= "AT1"
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19876..20910
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/gene= "megDV"
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/gene= "megBV"
                                                                                                                                                                                                                                                                                                                                                       'gene= "megA"
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gene= "megA"
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gene= "megA"
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21517..22053
/*tag= u
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3576..13791
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|3849..15126
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8268..19548
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/product= "megalomicin 6-deoxyerythronolide B
synthase 2"
/note= "polyketide synthase, encodes AAB82213"
22957...24237
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/gene= "megAIII"
/product= "megalomicin 6-deoxyerythronolide B
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/gene= "megAII"
/function= "KR3 (inactive)"
26998..27258
                                                                                                                                                                                                                                                                                                                         /*tag= aa
/gene= "megAII"
/function= "ACP3"
27393.28590
/*tag= ab
/gene= "megAII"
/function= "KS4"
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/gene= "megAII"
/gene= "AT3"
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//gene= "megAII"
/gene= "megAII"
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/*tag= ak
/gene= "megAIII"
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/*tag= ad
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/function= "KS3"
24544..25581
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/function= "ACP2"
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/function= "KR4"
33052..33312
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29953.30477
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33666..43271
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/function= "KS5"
24544..25581
/gene= "megA"
/function= "KR2"
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/gene= "megAIII"
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/gene= "megAIII"
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26230..26733
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/gene= "megAII"
                                                                                                    /gene= "megAII"
                    22318..22575
                                                                          22867..33555
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26230..26733
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28897..29931
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31396..32244
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32257..32799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding the human Pentraxin receptor useful for preventing, treating, ameliorating or detecting a disease associated with a neuronal disorder such as a stroke, multiple sclerosis, or
                                                                                                                                                                              Gaps
                                                                                                                                                         Length 47981;
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Rodes Gubern B, Adan Plana J, Puig CN, Carceller RA;
Masa Alvarez M, Piulats X, Den Daas I, Trullas OR;
DeGregorio-Rocasolano BN;
                                                                                                                                                                              Indels
                                                                                                                                                         DB 22;
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                                                                                                                                                                             Mismatches
                                                                                                                                                         Score 17.6;
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                                                                            "AT6"
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                                                          /*tag= an
/gene= "megAIII"
                                                                                                         'gene= "megAIII"
                            "megAIII"
                                                                                                                    "KR6"
                                      "KS6"
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                                                                                                                  /function="KH
31396..32244
/*tag= ap
                                              28897..29931
/*tag= an
        27393..28590
                                                                                                                                                         67.7%;
83.3%;
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                                                                            /function=
29953..3047
                                       /function=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alzheimer's disease
                                                                                                                                                                    Local Similarity
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         misc_feature
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                                                                                                                                                          Query Match
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pentraxin receptor (hPr) or a protein exhibiting biological properties of hPr and having a sequence selected from: (a) a fully defined 1853 bp sequence given in AAH4116; (b) a sequence which hybridises with (a); (c) a degenerate variant which deviates from (a) or (b); and (d) a fragment, derivative or allelic variation of (a), (b) or (c). (I) has neuroprotective, nootropic, cerebroprotective and cytostatic activity,

The present invention describes a nucleic acid (I) encoding the human

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from human breast and BT 474 cells. The method involves contacting from human breast and BT 474 cells. The method involves contacting from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater
and can be used in gene therapy. Pentraxin I, hPr, or hPr-encoding sequences are useful in the preparation of pharmaceutical compositions for preventing, treating or ameliorating a disease associated with a neuronal disorder such as stroke, acute head trauma, multiple sclerosis, spinal cord injury, Alzheimer's disease or brain tumour, or for providing a neuroprotective effect. The present sequence represents the human cDNA coding sequence of pentraxin I, which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New spatially-addressable set of single exon nucleic acid probes,
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                                                                                                                                                                                                                                            Score 17.2; DB 22; Length 1680;
Pred. No. 1.3e+02;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 4762; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human breast cell single exon nucleic acid probe #4762.
                                                                                                                                                                                     Sequence 1680 BP; 328 A; 571 C; 526 G; 255 T; 0 other;
                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABA46067 standard; DNA; 381 BP.
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2000US-0207456.
2000US-0608408.
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86.4%;
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21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                          Query Match 66.2°
Best Local Similarity 86.4
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease; cancer; ss.
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03-AUG-2000;
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ABA46067/c
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Conservative

80.08;

Best Local Similarity

20;

Matches

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diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
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                                                                                                                                                                                Length 381;
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                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human foetal liver single exon nucleic acid probe #4910.
                                                                                                                                Sequence 381 BP; 92 A; 130 C; 95 G; 64 T; 0 other;
                                                                                                                                                                                 Sequence 381 BP; 92 A; 130 C; 95 G; 64 T; 0 other;
                                                                                                                                                                                 65.4%; Score 17; DB 22; 80.0%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                  0; Mismatches
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2000US-0234687.
2000US-0236359.
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2000US-0608408.
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                                                                                                                                                                                             Best Local Similarity 80.09
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-483447/52.
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27-SEP-2000;
04-OCT-2000;
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30-JUN-2000;
03-AUG-2000;
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65.4%; Score 17; DB 22; Length 381;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single exon nucleic acid probes for analyzing gene expression in human
                                  Gaps
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                                                                                                                                                                                                                                                                   Probe #4686 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
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80.0%; Pred. No. 1.5e+02;
Live 0; Mismatches 5; Indels
                               Indels
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Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen W, Rank DR;
                                                                                241 CGGCCGAGGCGTTCAGAGTCCGGCC 217
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2000US-0608408.
2000US-0632366.
2000US-0234687.
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21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCI-2000; 2000GB-0024263.
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Best Local Similarity
These 20; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                               WO200157274-A2.
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30-JUN-2000;
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us-09-899-718a-5.rng

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microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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                                         WO200157276-A2.
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30-JUN-2000; 2
03-AUG-2000; 2
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                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                     Single exon nucleic acid probes for analyzing gene expression in human
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                                                                                            Human brain expressed single exon probe SEQ ID NO: 4740.
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                               AAK04749 standard; DNA; 381 BP
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2000US-0234687.
2000US-0236359.
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2000US-0608408
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                                                                       05-NOV-2001 (first entry)
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Matches 20; Conservative
                                                                                                                                     epilepsy; cancer; ss
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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30-JUN-2000;
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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
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2000US-0207456.
2000US-0608408.
2000US-0632366.
                                                      04-FEB-2000, 2000US-0180312.
26-MAY-2000, 2000US-0207456.
30-UUN-2000, 2000US-0603408.
03-AUG-2000, 2000US-0532366.
21-SEP-2000, 2000US-0234687.
27-SEP-2000, 2000US-0234687.
04-OCT-2000, 2000GB-0024263.
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30-JAN-2001; 2001WO-US00668
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Best Local Similarity 80.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-488900/53.
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Gaps

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Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                         Query Match
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                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe #4913 used to measure gene expression in human placenta sample.
                                                                                                            Human genome-derived single exon nucleic acid probes useful for
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                                                                                                                         analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                    Query Match 65.4%; Score 17; DB 22; Length 381; Best Local Similarity 80.0%; Pred. No. 1.5e+02; Matches 20; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                      Sequence 381 BP; 92 A; 130 C; 95 G; 64 T; 0 other;
                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                            Claim 25; SEQ ID No 4804; 487pp; English
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                                                                 Hanzel DK, Chen W, Rank DR,
                                                                                                                                                                                                                                                                                                                                                                           241 CGGCGAGGCGTTCAGAGTCCGGCC 217
                                                                                                                                                                                                                                                                                                                                                                2 ccgtctaggcgttcggtgtccggcc 26
                                           (MOLE-) MOLECULAR DYNAMICS INC.
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2000US-0207456.
2000US-0608408.
21-SEP-2000; 2000US-0234687. 27-SEP-2000; 2000US-0236359.
                        2000GB-0024263.
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2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genetic disorder; ss.
                                                                                      WPI; 2001-488901/53.
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21-SEP-2000; 2
27-SEP-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                      04-OCT-2000;
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                                                                  Penn SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAI36227;
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Probe; human; breast disease; breast cancer; development disorder; ss; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
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                                                                                                                                                                                The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful
                                                                                                                                                    The present invention relates to single exon nucleic acid probes (SENP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to novel single exon nucleic acid probes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probe #4649 used to measure gene expression in human breast sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                                                                                                                                    for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 381 BP; 92 A; 130 C; 95 G; 64 T; 0 other;
analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                Claim 25; SEQ ID No 4913; 654pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 CGGCCGAGCCGTTCAGAGTCCGGCC 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 ccgtctaggcgttcggtgtccggcc 26
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30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-053366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Conservative
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Looker DL, Rosendal MS,
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Hoffman SJ,
                                                                                                                                                                                                                                                                               AAH35021;
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                                                                                                                                                                                                                                                    RESULT
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                              Gaps
                                                                                                                                                                  Polycistronic operon for coexpression of (des-Val)-alpha-(Gly-Gly)-alpha globin and des-Val beta globin.
                                                                                                                                                                                        Polycistronic operon; di-alpha-globin; di-beta globin; haemoglobin;
                                                                                                                                                                                                                                                                 'product=(des-Val)-alpha-(Gly-Gly)-alpha globin
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                                              Query Match 65.4%; Score 17; DB 22; Length 381; Best Local Similarity 80.0%; Pred. No. 1.5e+02; Matches 20; Conservative 0; Mismatches 5; Indels
                           Sequence 381 BP; 92 A; 130 C; 95 G; 64 T; 0 other;
                                                                                                                                                                                                                                                                                                           *tag= c
product=(des-Val)-alpha globin
                                                                                                                                                                                                                                                                         190..1012
/label=cotranslational coupler
                                                                                                                                                                                                                                              'label=cotranslational coupler
                                                                                                                                                                                                                                                                                      1019..1457
/label=des-Val beta globin
                                                                                                                                                                                                                                                                                                                                      product=Gly-Gly linker
                                                                                                                                                                                                                                                                                                                                                          product=alpha globin
                                                                                                                                                                                                                         Location/Qualifiers
                                                                         BP.
                                                                                                                          AAQ06685 standard; DNA; 1463
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89US-0374161.
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1005..1012
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72..77
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976..980
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                                                                                                                                                                                                            synthetic
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                                                                                                                    AAQ06685
                                                                                                            RESULT
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Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
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                                                                                                                                                                                                                                                                                                                                                                       This polycistronic operon contains the di-alpha and beta-globin genes in separate cistrons, both preceded by a short cotranslational coupler region. The di-alpha-globin gene is transcribed first as it affects folding of the beta globin. This is essential for incorporation of the haem molecule to form functional haemoglobin. The 2 alpha-like polypeptides encoded are nearly identical and sepd. by an interposed Gly-Gly linker. The synthetic haemoglobin produced on transformation of host, eg. yeast, cells has an increased intravascular half life. The 5' end overhangs the 3' end of the complementary strand by AATT and the 5' end of the complementary strand by AATT and this sense strand by TCGA. See also AAQ06684.
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                                                                                                                                                                   Di-alpha and di-beta globin-like polypeptide(s) - used for prodn. of haemoglobin having increased half-life and produced in
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Stetler GL, Wagenbach
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80.0%; Pred. No. 1.6e+02;
...wismatches 5; Indels
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                                                                                                         P-PSDB; AAR08114, AAR08115
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Best Local Similarity 80.0%
Matches 20; Conservative
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                                                                        WPI; 1990-361480/48
                                                                                                                                                                                                                                            bacteria and yeast
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CC cancer-associated nucleic acid molecules (N) and proteins (P), where
CC the proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene
CC therapy and vaccine production. N and P may be used in the prevention,
Cd diagnosis and treatment of diseases associated with inappropriate P
CC expression. For example, N and P may be used to treat disorders
CC in a patient's genome that affect the activity of P by expressing
CC in a patient's genome that affect the activity of P by expressing
CC inactive proteins or to supplement the patients own production of P.
CC Additionally, N may be used to produce the colon cancer-associated Ps,
CC by inserting the nucleic acids into a host cell and culturing the cell
CC express the proteins. N and P can be used in the prevention, diagnosis
and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC and AAB377789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2443 BP; 612 A; 571 C; 599 G; 659 T; 2 other;
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2 ccgtctaggcgttcggtgtccggcc 26 ||| ||| ||| ||| ||||| ||||| 130 ccgmctagccgtgcggtgccaggcc 154 g δ

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Gaps .; 0

Length 2443;

Query Match 65.4%; Score 17; DB 22; Length 24 Best Local Similarity 80.0%; Pred. No. 1.6e+02; Matches 20; Conservative 0; Mismatches 5; Indels

Search completed: July 31, 2002, 14:11:22 Job time: 17379 sec

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AX349067 Sequence AX349063 Sequence AL138538 Streptomy AF079762 Streptomy AC005929 Leishmani AC005929 Leishmani U96127 Canis famil

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AL136502 Streptomy AC098934 Homo sapi

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AC109873 Rattus no AL049768 Leishmani AC105239 Homo sapi AL353822 Neurospor AL451020 Neurospor AL606557 Oryza sat AE008357 Agrobacte AF016585 Streptomy AF263245 Micromono AX112026 Sequence AP001141 Homo sapi AC103175 Rattus no AC084775 Homo sapi AC03175 Homo sapi AC079366 Mus muscu AC079366 Mus muscu AC103125 Homo sapi AC079366 Mus muscu AC1031254 Homo sapi AC079366 Homo sapi AC079366 Homo sapi AC079366 Homo sapi

AF319543 Streptomy AC109873 Rattus no AL049768 Leishmani S.lincolnen

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1 (sites)
Sprunck,S., Kluth,A., Becker,D., Luetticke,S. and Loerz,H.
Promoters of gene expression in plant caryopses
Patent: WO 0202785-A5 10-JAN-2002;
Aventis CropScience GmbH (DE)
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/db_xref="taxon:32630"
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Sequence 5 from Patent W00202785.
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    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Database

AX13778 Sequence
AX14774 Sequence
BC018289 Homo sapi
AL10278 Homo sapi
AF006013 Homo sapi
U49262 Human dishe
U7561 Human dishe
U61849 Human neuro
D86663 Human mRNA
X18862 Streptomyce
AL646077 Streptomyce
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PAT 06-FEB-2002

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Description

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Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABC transporter ATP-binding protein; globin; kinase; lipoprotein; membrane protein; O-methyltransferase; protein kinase; secreted protein; secreted sugar-binding protein; sugar hydrolase; sugar transport inner membrane protein; sugar transport system permease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
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Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacterides;
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Aventis CropScience GmbH (DE)
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Sequence 1 from Patent W00202785.
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HPFOGTSOYAMQLDGEWKLGMAKDGYDFEIGTPAPWYADDBAAPKGFELSGTYWGIA
PQSKKQNAAWELVKYMTDTGAYVARANA TRNVESTFPALKSPDLKTDPEFKYFLDIA
QHREENSPPASVNOATYQLTLQDLGYQYESGKVKDLKAGLEKAAAQLDRDIEQAK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              correct initiation codon. Where possible we choose an initiation codon (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most uppstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MKAPPKTWSEFAQVAKKLTKTKGDGYRQLGFMPNYHGYETVVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.

The length in codons is given for each CDS.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.

Where these have been used to deduce the initiation codon. Usuang a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibbe et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="nominal overlap with S. coelicolor cosmid St8E4A"
                                                                                                                                                                                                                                                                                                                                  (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S.
coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                       Streptomyces coelicolor sequencing at The Sanger Centre is funded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 as overlap and to SW.WALK_STRPN (EMBL:L08611)
Streptococcus pneumoniae maltose/maltodextrin-binding
protein precursor MallX, 423 as; fasta scores: opt: 184
z-score: 217.6 E(): 0.0001; 22.9% identity in 279 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid 6D10 Overlaps with cosmid C61 on the AseI-C genomic
CBIÓ 15A E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof.
David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                     by the BBSRC and Beowulf Genomics, Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMPORTANT: This sequence MAY NOT be the entire insert of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative sugar-binding protein" /protein_id="CAB71196.1"
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/strain="A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION:
correct initiation codon. Where po
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/note="SC6D10.04, possible sugar hydrolase, len: 421 aa; similar to SW:CELF_ECOLI (EMBL: X52890) Escherichia coli 6-phospho-beta-glucosidase (EC 3.2.1.86) CelF, 450 aa; fasta scores: opt: 556 z-score: 624.0 E(): 2.4e-27; 36.0% identity in 431 aa overlap and to SW:AGAL_ECOLI (EMBL:X0484) Escherichia coli alpha-galactosidase (EC 3.2.1.22) (mellbiase) MelA, 451 aa; fasta scores: opt: 303.2.1.22) (mellbiase) MelA, 451 aa; fasta scores: opt: 305 z-score: 338.4 E(): 1.9e-11; 25.5% identity in 459 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VGĽCNVAIGLQRKFAALLGVAPADVHLDHVGLNHLTWETGVRLGGPEGEDVLPRLLAE
HGENVAADLKLPRPLLDRIGVVPSYYLRYYYAHDEVVDELRRYFSRABVABVBRQLL
OWEDVALDERFPALLAKRGGAYYSEAAVDLAAALLGGAGSPYQVVNTYNRGTLPFLPD
DAVIEVPAAVGGKGAAPLPVADVDDLYAGLAAALLGGAGSPYQVVNTYNRGTLPFLPD
AHPLVGQYAYAEQLTDRLIAHNREHLAMA"
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VGQETTGAGGLAKALRTVPVVLDIAERVRRANPDAWIIDFTNPVGIVTRALLQAGHRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MKLTVVGGGSTYTPELIDGFARLRDTLPVEELVLVDPAADRLEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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Minnesota, 420 Delaware Street SE # 1060, Minneapolis, MN 55455,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Xue, Y., Zhao, L., Liu, Hw. and Sherman, D. H.
A gene cluster for marcolide antibiotic biosynthesis in
streptomyces venezuelae: architecture of metabolic diversity
proc. Natl. Acad. Sci. U.S.A. 95 (21), 12111-12116 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                              /product="putative sugar hydrolase"
/protein_id="CAB71199.1"
/db_xref="G1:6855385"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 2e+02;
0; Mismatches
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/gene="SC6D10.05"
4000..4017
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                         /gene="SC6D10.04"
                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/transl_table=11
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/trans1_table=11
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91.3%;
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                                                                                                                                                                                                                                                                                                                overlap"
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Best Local Similarity
Matches 21; Conserv
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KEYWORDS
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(EMBL:AL122662) Streptomyces coelicolor probable sugar transport inner membrane protein SCF11.20, 299 as, fasta scores: opt: 662 z-score: 806.9 E(): 0; 38.4% identity in subtliss probable ABC transporter permease protein Sc811.20, 299 as if as a subtliss probable ABC transporter permease protein FeSO, 296 as; fasta scores: opt: 588 z-score: 17.5 E(): 1.5e-32; 33.2% identity in 304 as overlap. Contains Pfam match to entry PF00528 PDL.transp.

Binding-protein-dependent transport systems inner membrane component. Contains possible hydrophobic membrane spanning
                   /gene="SC6D10.02"
/forte="SC6D10.02, possible sugar transport system permease protein, len: 314 aa; similar to TR:09x6c4 (EMBL:AF13538)
Thermus brocklanus putative integral membrane protein
BdfF, 280 aa; fasta scores: opt: 498 z-score: 582.4 E(): 5e-25, 35.4% identity in 288 aa overlap and to
SW:LACF-AGRND (EMBL:X66596) Agrobacterium radiobacter lactose transport system permease protein LacF, 298 aa; fasta scores: opt: 437 z-score: 511.6 E(): 4.4e-21; 31.1% identity in 315 aa overlap. Contains Pfam match to entry PF00528 BPD_transp, Binding-protein-dependent transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKPALTALAVWGVGDLMVIFMAALLDVPKEQYEAAELDGASAWQRFRFVTLPNISPIV
LFAVVTGVIQTWQYYTQPLVAGKVASGIIGGSGQSFEPGYPDKSTLTLPQLVYNLGFQ
RFDYGSACVVALVLFALAMAFTALLMRRGGLIQAGDR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1376. .1654
/gene="Sc6D10.02"
/note="Pfam match to entry PF00528 BPD_transp,
Blinding-protein-dependent transport systems inner membrane component, score 59.00, E-value le-13"
1379. .1465
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LSGTLWPLIVPMAFGDAFSIFLLRQFLLTIPDEYLDAAKVDGGGELRTLLRVVLPMAK
PGIAAVALFQFFYAWNDYFGPQIYASENPGAWTLSYGLESFKGAHHTDWNLTMAATVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1379. .1465
Agene="SC65010.02"
/note="PS00402 Binding-protein-dependent transport systems
inner membrane comp sign."
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/protein_id="CAB71198.1"
/db_xref="GI:6855384"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fprotein_id="CaB71197.1"
/db_xref="G1:6855383"
/translation="MATNTLRAKRRSSALRTAAFMSPWLVGFAVFFAYPLVSTVYFSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MKYDGFGVPQFRGLENWAYVFQDYPLFWPALRNTLWLVLVWYTCRVVFGLGVGLLITK
IRTGAGVFRTLFYLPYLAPPVAATLAFVFLLNPGTGPVNSVLEGLGVPAPGWFTDSAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MTTQVPTAQVPARPAAAGSPPPTEERTARRRVLLHWIAVHSLGV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAALFFTLPFVFVVLTSLMSDQQALTRDLWPHTWEWGNYRAVLDTPGFLTWWKNTLLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="SC6D10.03"
1771. 2682
/gene="SC6D10.03"
/note="SC6D10.03, possible sugar transport inner membrane
                                                                                                                                                                                                                                                                                                                                                                 systems inner membrane component and match to Prosite entry PS00402 Binding-protein-dependent transport systems inner membrane comp sign. Contains also possible N-terminal region signal peptide sequence and possible hydrophobic membrane spanning regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative sugar transport system permease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="Pfam match to entry PF00528 BPD_transp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VMAPVILVFFFAQKAFVEGVTLTGVKG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="SC6D10.03"
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/transl_table=11
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FHLLANNDSMVDDLVDFARSWQPDLVLWEPTTYAGAVAAQVTGAAHARVLWGPDVWGS
ARRKFVALRDRQPPEHREDPTAEWLTWTLDRYGASFEEELLITGQFTIDPTPPSLRLDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MYEVDHADVYDLFYLGRGKDYAAEASDIADLVRSRTPEASSLLD
VGCGGGTHEHFTKEFGDTAGLELSBODLTHARKLEDATHGGDMRDFRLGRKFSAV
VSMSSSVGYLKTTEELGAAVASFABELEPGGVVVVERWWFPETFADGWVSAVRRDG
RTVARVSHSVREGNATREEVHFTVADPGKGVRHFSDVHLITLEHQAEVEAAFTAAGLR
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anvQytsraaelvaqwtldekisfvHwaldpdrqvnvgylpgvprlgipelraadgpng
irlvGqtatalpapvalastfddtwadsygkvwgrdgratalwgdwylgpwmnirvphg
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REIEFPAFEASSKAGAASFMCAYNGLNGKPSCGNDELLNNVLRTQWGFQGWVMSDWLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPGTDA ITKGLDQEMGVELPGDVPKGEPSPPAKFFGEALKTAVLNGTVPEAAVTRSAE
RIVGQMEKFGLLLATPAPRPERDKAGAQAVSRKVAENGAVLLRNEGQALPLAGDAGKS
IAVIGPTAVDPKVTGLGSAHVVPDSAAAPLDT IKARAGAGATVTYETGEEFFGTQIPA
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TAVVFAYDDGTEGVDRPNLSLPGTQDKLISAVADANPNTIVVLNTGSSVLMPWLSKTR
                                                                                                                                                                                                                            ALAELTALLADSDDSPGALLSALGVTAAVQLTGNAVLALLAHPEQWRELCDRPGLAAA
AVEETLRYDPPVQLDARVVRGETELAGRRLPAGAHVVVLTAATGRDPEVFTDPERFDL
ARPDAAAHLALHPAGPYGPVASLVRLQAEVALRTLAGRFPGLRQAGDVLRPRRAPVGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLPTVGMRYVPYNGTSVVPDMLSEPPARPRVCLTLGVSAREVLGGDGVSQGDILEALA
DLDIELVATLDASQRAEITRYPEKHTFFDFPPAHALLESCSAIIHHGGAGTYATAVIN
AVPOYMLAELWDAPVKARAVAROGAGFFLPPAELTPQAVRDAVVRILDDPSVATAAHR
LREETFGDPTPAGIVPELERLAAQHRRPPADARH"
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                                                                                                                                                              GVPVPQQVLSYGEGCPLEREQVLPAAGDVPEGGQRAVVEGIHRETLEGLAPDPSASYA
FELLGGFVRPAVTAAAAAVLGVPADRRADFADLLERLRPLSDSLLAPQSLRTVRAADG
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                                                                                                /translation="MTDDLTGALTQPPLGRTVRAVADRELGTHLLETRGIHWIHAANG
                                                                                                                                  DPYATVLRGQADDPYPAYERVRARGALSFSPTGSWVTADHALAASILCSTDFGVSGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation-"MRVLLTSFAHHTHYYGLVPLAWALLAAGHEVRVASQPALTDTIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y REGIHVGY RWFDK ENVK PLFPFGHGLSYTSFTQSAPTVVRTSTGGLKVTVTVRNSGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="N,N-dimethyltransferase"
/protein_id="AAC68678.1"
/db_xref="G1:3789895"
   tautomerase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="glycosyl transferase"
/protein_id="AAC68677.1"
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/protein_id="AAC68679.1"
/db_xref="GI:3789896"
/product="putative tauton
/protein_id="AAC68676.1"
/db_xref="GI:3789893"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(6143. .7282)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="GI:3789894
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/transl_table=11
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/transl_table=11
                                                                                                                                                                                                                                                                                                                     GPLSVPVSSS"
1475. .2755
/gene="desVII"
1475. .2755
/gene="desVII"
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/gene="desVI"
2845. .3558
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/gene="desVI"
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/3625. FF
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/gene="desR"
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/db_xref="G1:3789901"
/translation="MKSALSDLAFFGGPAAFDQPLLVGRPNRIDRARLYERLDRALDS
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/db_xref="G1:3789899"
/translat_ton="MKGIVLAGGSGTRLHPATSVISKOILPVVNKPMIYYPLSVLMLG
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ALTLGDNIFHGPGLIFTEQSLLGNGRHLGIELDYAVOKEPAGTADALLVGAEHIGDDTC
ALTLGDNIFHGPGLITTLLRDSIARLDGCVLFCYPVKDPERYGVAEVDATGRLTDLVEK
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FAWLDTGTHDSLLRAAQYVQVLEERQGVWIAGLEEIAFRMGFIDAEACHGLGEGLSRT
EYGSYLMEIAGREGAP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ÓWLSNGGPLVREFEERVAGLAGVRHAVATCNATAGLQLLAHAAGLTGEVIMPSMTFAA
TPHALRWIGLTPVFADIDPDTGNLDPDQVAAAVTPRTSAVVGVHLWGRPCAADQLRKV
                                                                                                                                                                  /translation="mSSRAETPRVPFLDLKAAYEELRAETDAAIARVLDSGRYLLGPE
LEGFEAEFAAYCETDHAVGVNSGMDALQLALRGLGIGPGDEVIVPSHTYIASWLAVSA
                                                                                                                                                                                                                                                                     TGATPVPVEPHEDHPTLDPLLVEKAITPRTRALLPVHLYGHPADMDALRELADRHGLH
                                                                                                                                                                                                                                                                                                                                           IVEDAAQAHGARYRGRRIGAGSSVAAFSFYPGKNLGCFGDGGAVVTGDPELAERLRML
                                                                                                                                                                                                                                                                                                                                                                                         RNYGSRÖKYSHETKGTNSRLDEMQAAVLRIRLAHLDSWNGRRSALAAEYLSGLAGLPG
IGLPVTAPDTDPVWHLFTVRTERRDELRSHLDARGIDTLTHYPVPVHLSPAYAGEAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mrllvTgGaGFIGSHFVRQLLAGAYPDVPADEVIVLDSLTYAGN
RANLAPVDADPRLRFVHGDIRDAGLLARELRGVDAIVHFAAESHVDRSIAGASVFTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NVQGTQTLLQCAVDAGVGRVVHVSTDEVYGSIDSGSWTESSPLEPNSPYAASKAGSDL
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HTDDHCRGIALVLAGGRAGEIYHIGGGLELTNRELTGILLDSLGADWSSVRKVADRRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGSLPRAESFARQVLSLPIGPHLERPQALRVIDAVREWAERVDQA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product."TDP-glucose-4,6-dehydratase"
/protein_id="AAC68681.1"
/db_xref="GI:3789898"
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/protein_id="AAC68683.1"
/db_xref="G1:3789900"
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/protein_id="AAC68680.1"
/db_xref="G1:3789897"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(9495. .10952)
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complement(8424. .9302)
/gene="desIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(8424. .9302)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(7279. .8292)
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/product="4-dehydrase"
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ARIRALHNFGFDLPGGSPAGGTNAKMSEAAAAMGLTSLDAFPEVIDRNRRNHAAYREH
LADLPGVLVADHDRHGLNNHQYVIVEIDEATTGIHRDLVMEVLKAEGVHTRAYFSPGC
HELEPYRGQPHAPLPHTERLAARVLSLPTGTAIGDDIRRVADLLRLCATRGRELTAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC005928 37969 bp DNA linear INV 24-FEB-2000 Leishmania major chromosome 3 clone L6290 strain Friedlin, complete
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PQPKQWRERRHSSSIANSPSRSASSASHASHIDAYEVAVABETRTDVGGSLLQQP
TSLPSCTVKSYGTASDISDDGSRSSLSAVAVAVHYANTFDLMTQTVGYRTPSTRAEV
OPGQLEHHAQHPQQRQGQVMSSYAVEFSAYDPHSFTLLLGNAHHVGGYGQSEPAPLAR
ADEHGLRLYFDAAHALGCAVDGRPAGSLGDAEVFSFHATKAVNAFEGGAVVTDDADLA
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VELVMRRVGSTSLLQFLMVVLLVVMLLVGNAFQVIFLNFWIHQFPTKLNPQIAPASSS
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Cawthra,J., Marsolini,F., Sunkin,S. and Stuart,K.D.
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Submitted (24-FEB-2000) Seattle Biomedical Research Institution, 4
Nickerson Street, Seattle, WA 98109-1651, USA
On Feb 24, 2000 this sequence version replaced gi:6425646.
Location/Qualifiers
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                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                            71.5%; Score 18.6; DB 1; Length 12441; 84.0%; Pred. No. 7e+02;
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/db_xref="G1:7025826"
                                                                                           HRDTAPAPLAAPQTSTPTIGRSR'
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                                                                                                            4686 g
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AC005928.4 GI:7025823
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WLRMRLATAEEAAEPVSAAERGSNEVTPDTSDTFFRGGADVVÄGPASPLDADCAKVAS
SIARVNDRTLANGLEDEEDDREELRARPARHAKTKLANSVRPSSVDANDDAVGDST
SAHEPVASDSSDGTASGGVAITPAASPDEPATSRVNEBGAVHDLSGVEBGETLRFTAT
GAPPLPTRTMFTVRYNGGEDTVVKLVMLAGETVIQLCFTLCLIPADALPWGNSETVS
ATLDNFARGIRCVFTIRDNFLYCELYTIGFVETVYGCATURYSAALCSIVTGLSSVY
TALANFARGIRCVFTIRDNFLYCELYTIGFCVETVYGCATURYSAALCSIVTGLSSPY
TALANFAGGEDVANGVDGDSPWYYNMFAIFFLCVAALIYVWMEEMTDAEKVQAEYEKM
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YAASALLDRWCLFGEAAAVVPSMPASSGATLDGTQQSQRPHDAAAHHLRIAELALGAG
LLSNYRAVWLNGAVLSHPGTARSVLVVGPRRSGKTTLALHCLSAAAMQASSSASGDGG
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LAAAVELPSFLÜCGEAGLRACHENTDOVLMDMSKTYRVRLEDIYRASSPDISTOMAPVV
VAGAVULLDMNVEELASASPTPVRAVREIPLHDGGVEELLKRAQDYMFHGHHLLR
TVYDARQDAARLADALADEMDTAQPRSLANGTAPALHGIEGSVNFDLATOLLINSLLS
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DMRALLEQDINGIDYIAFCSRCAVDSLSAALDHRYGGGGESVSERAGSAPAVNEDRRA
TAVVKVLAKCALAAIGKDADYVFERLRIRTTICPDEPSPAGIAAKLAESGRABGRTIA
                                                                                                                                                                                            HQQHIPHSEHLLHGEDASVKLVMLTSDTAIQAILAVVLMPMDALPWFGGSHSIREVVQ
NLDEGIDCVLHCPRNMRYCILYSTGFVLVYIASAYLNRYSVTLCSMVSQLSGPITALV
                                                                                                                                                                                                                                                                       LIAFPTLNMTDDASPWYVSVFAIFLLSCGTVLYVYWDEMTVEEKÄVGEMOLKWAMMOE
OSPRHAPSLABGQRYHEVDSGVNGSSLATSQSGVSQPQQQQHRHARSRRYCRRRQSGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTLMRSLPSRTASVVMPSLRAFRERLCKMSLTQILMIILLVALVMVGNFMQIVMLNFW
LISFPSDGTPGNYTAFAVPGIFFAVLFVLLLGAYTAIRRPSLRFARHAHGWVILIGVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FCDAFNSWLATYAASYTSEVLQALFSNLCPLXAVFLCKWILHDTRRYANVYIVSVFVL
TICGILAASLYGLIKDHNMGEGKWWILIFFLSMPFRVLMNVWQSLYMIVYTHDPNFVL
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THVLASTRVSAHVGPPAPPLGYPDYIALEATQHTEGVLRGETYAYHHAAAVGAVPAPP
                                     AGWRLLFGIGAMDALNSALAIYAAANTPEVLQALFVSLVPIYSAIFTKWLLKDPRDYA
NPYVVVSFVLIATGVALASLFNQVVTHHHTFEDRSGSGHAGVKELLVAVFSDGSSSSL
                                                                                                                     SPVALDRRLWCFIFFLSVPPTVLMNVWQTMYMIRYTSNDQLMAYLAEHADEAECGESS
                                                                                                                                                          NDVAAGAPGQSTPLLDSARDSHGDAHHCPSPAAGEAVERVPLQPSVVSVSRSLPHGWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MSPIHRKHMEVLGLGVKGTANDASNTQRPAGALSREEEQLPRES
SLTTGATAAAAAAASGDVRHGPLPEEDDLSNATVVLAAAAETTATRPPIFGSGLRRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDALASLPLRHLLIRGSSFASPLRITSVCLEPCHTPGAEETAAATRMTAPAHDAGANV
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GVAFTSAGELAVLLRRSPQCLMNIDVACFGPYTAGFAAKHGVKVSCVAKDFRSFDGFA
SASSGSGTDSSSGRHAEALASSYTTFVISAVLFPAFFVVLLITYALWRRPNLRFTREW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="predicted using Glimmer, Testcode and CodonUsage; Glimmer predicts start codon at 4496" 4472...6754 /gene="L6910.6"
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Glimmer predicts start codon at 19287"
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/gene="HEL2"
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/db_xref="G1:7025828"
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/db_xref="G1:7025829"
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/db_xref="GI:7025827"
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/gene="L6290.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /qene="L6910.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="L6910.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="L6910.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATIEQHYASR"
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/note="L6290.2; L6910.1L; predicted using Glimmer,

PPPPPPPPPPALFYAQRKECVLVLDSSRVEMSEDTHVYRLMPNFHAAAAAATRGWQR

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TDVNISWQDVVGDESAIITGGALSALPDVILAEPKKAMKYPHLTHDLIDQLARAFRVE
GHVSNRPYPATLGNANELGGWIVSQPFDELNDVVDAYVERESQRNVTERERRKQLAME
AAFVTDAAQQAESMGIRGFTAGTLAVVCSDSDEDEAAAATDGAAGTSAGKVAKKVKQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTAAITRATGTSFGRNEDPGEVLKDGSAVPLOLTMWRLLVDASGWREAELAFTITDDD
ADRSPAADKKRRKSAKDKRATNLYAFGLIADLVEENITNAKSGSHGSDDWGKLERLRK
VKKDFTVYDATSYLNWVYLTYVQLHFQCKLMTRVVRLQLMQWKNERERARQAQEAPNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILTLEQLQSGFPPDITLVPSEVVQLYQKMCTLFTEHVFAKWSKVAIVQAMKAQLSMLL
PETYFQQEIYITQQRARQYEADVKNAFAYWVYLNKGCDADGLETLSEGEVVAFNTDMR
ELCETILQSFSQRLREDEAQLDKYATDAALKPEGRPVDTSAAEAEATASDTATAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRAGRRGLDYLGHLIFLSVSMKKITRLMTSSMTVIKGNVQVDPITQLRLLQLYDYARH
RDLKGAEEWSRRALGMAERLYVNPLFFAGRAAMENGNMESFTVEFAQMLLGFLHREGL
HFKDRPSSLGSLLVDAMYVFRNAQVGVEGFAFISMITRKVPAKARLARRFRYLAPSDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVVQEAKAELLAYLESVNKVCGVPLELHRSALSDPAVIELWSGRRVAKQHRVVLAPLD
VCSPATKPFSYVSVFRMISAFYTYLASTLKEPADTRLPYMCAKTKKKHCIFGGTSDMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="SRHRRPSRHMEPSASATTLAAADAAPQSAAATSSPHVHRHDTTA
TSSPAPPTQPSSSLTSSGAGDKVRATAERVGGREVAPRAVASSRDGSNGARTSDRSTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEDKYSAADSTTPDTPADRDRVGASPKYSGSAFPSLPAPLQQRTPSTRTÄTPPPSSSA
STSVFAPVMNAERVLRARPPALWHVAYAPTHPHTAASCGKVQLLQQRVAELWIPFTLL
PPPPSISGSSTAVSGIPATSSAEESQVTQVLRLAEAGVSCERGAADSAAAPLPLEVHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEFLIMSDGEQLGHETELMHLFHNHTEEELLRFEKEGGIGEEGTPASAASATPLTDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSAVSVLPPSHRPRQKACFETPEMMQLMTMGHLLERPVIPTKDYRVVFNPDGWQRELL
DIVDNRGSAVVCAPTSAGKTFISÎYCMYSALKTSNTKVVVYVAPNRALINQAVADVCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VILDEIHTMESSGNGDVWERVLALLPCPFVALSATLGETQQLCGWLNRVQQRLEAQQP
EAAKRDFTVHDIPSSGSIQRWNDIKKYMYLPPPGYHPQLKKLTAKYPNRYIHDLHPLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IAQPRKAFFPESKEFIADNIISVLRELNSRDMGPTIVFTFEGEDCDDLTKAIIARLED
AEAAYRQTEEFAQYKATMERKAAAAEAARRQRESTLKQKKLTTDDGGEVDRADRDVDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NMNDDEDYVVPDVLPEFTFIGGYCTVDPIVVKEAVEECIKRGDTLCARAIQRGVGIHH
AGVKGKLRRMMEILFRGRHCGVICATETLALGVHSPCRSVVLAGDHVLLNTTQFRQMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQQQQQQSDDDANSVPTATTPQPYNDFOCRLVALGEARRPPLTSEGHMALPENADGAG
VAVPQVNDPSQPLARPQTSAFASPPPPTAATGGSRRRARMPLVFVVAPRLIASFIHHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VDGGGSSALAAAYSEEEHQLGMEYIRRAHPHLFRRYVGPLSESASAARDGMPSLPVSS
ESRGGLSASANPNIAAAAATGGGMVQRNHRDMYFDSGSAVTATGSDSVRPSASPHSAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATTTPSLMGFGTGHGRGSSGALAPHVLRDVSHLNTAVYDALVATYAPPSEPSPVSPP
PPLCPTLGQQQPRPTAATAKPVVMLLDSPALLADAEGVRLFQSGVRGVQQAVVSTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGDAGDNVQEARVACVLRNVRVSATAARKFSSTVNPLLNASNGGSPSTTQRTSLRFSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QSSTAPSPAGDVHTCHLPRGLTLHCRNMYLYGHLRVFGNLVLDSCVFVGSLTTEELAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VQVSRSHLALMPDDRLLLRQPPYRRGPSDRCRGAGRGAPRQRASSTASPGAADAARPP
                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MSSHYRELNQLFVDANGQPDFDATVEISASLPIKQLFQERSLLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVGQIDSLQSPDECRMAWKFLATFAGQPAALVCIDKALTEVAVDFHYAMARPRQFDMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VHLSAMEKFFIDGDSLLMAALSSPHVDWDLMQPLHVLHNAQVLLRGLQSRGGHFHIVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRHTAWFWEPTPQKLFIREALRETLTAVAATNPDSRLVVDTFDSFHSEEFAAYVSKYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRENAVVVFAVTVSSGNFARSLVLEPNSTKLAAALERAVPLPTLSDASLALTKDGQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RREQVVSAAVHAYLHAGDSTPPRTEQQRQLCQVMVTTAYCTALVSAELRAQRSVTSPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSGQKNKKARSREDIIREEANLRDANKTVQDWTQQVAELCKKTDQASRLTDVADSIGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NVGVPLFLYCHHKVLACIRDNGVAISTDDLDAVRSALAHFDFPASYYEKVDGAIAKWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RYGSKKYSFPGRNVYGVHGGADYHRYVDSCQVLVTLPEVLETLLLSPKYKEWAKRLDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RHDGAQVLINACITDFVRCKAQIDSVRSNFRFTLLEELNGLSQSESYAVLNQTERLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALCSLELMSQDWELTPENMVLLLIALFETLNPFAGDGRVSVDDAERMEHLRETVAAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                              PSSSNSEATAASNASPSTVKPVHETTALLRTCNAVLRWAAAEKAGQDQGGAAVAARAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLELKORITEDOTMELKRPYRSLVDDESHGDTVAFYYHCFLTWATARRIKVAYSSRII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAAFLNEMAPYLLQAFQHCDCATGRGTEFDVYDGHLITIMAHLLRTTPAEQLLDEDGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LMAKLKETAEPYAARDPFVAISGCGDHFVHSEDLVTTLRRGLFCDRRMLPVLDLTDGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NISGLTRDDKYTPLQVLSALYPERERGENVABEDLKFYAGTLGVMDFASQLHELRPHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  //orte="L6290.3R; predicted using Glimmer, Testcode and CodonUsage; Glimmer predicts start codon at 15410" complement(29757. .>37969)
                                                                                                                                                   /note="Blastp similarity to helicases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(29757. .>37969)
/gene="L505.2"
                                             complement(22336. .28971)
                                                                                                                                                                                                                                              /product="Helicase 2"
/protein_id="AAF35923.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAF35924.1"
Testcode and CodonUsage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DKELAMVQWMARIAEMRRARK"
                                                                                                                                                                                                                                                                                                                                              /db_xref="GI:7025824"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="GI:7025825"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="L505.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="L505.2"
                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=3
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                                                                                                                                                                                                                                                                                                     AC005929 41944 bp DNA linear INV 24-FEB-2000 Leishmania major chromosome 3 clone L6910 strain Friedlin, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myler, P.J., Sisk, E., Hixson, G., Kiser, P., Rickel, E., Hassebrock, M., Cawthra, J., Marsolini, F., Sunkin, S. and Stuart, K.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myler, P.J., Sisk, E., Hixson, G., Kiser, P., Rickel, E., Hassebrock, M., Cawthra, J., Marsolini, F., Sunkin, S. and Stuart, K.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myler, P.J., Sisk, E., Hixson, G., Kiser, P., Rickel, E., Hassebrock, M., Cawthra, J., Marsolini, F., Sunkin, S. and Stuart, K.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YDGVGQATFAGSLSVLRPRGYMITFGNASGAVPPVSPLELSRAGSVYLQRPTLGDFMR
TPEEVQRRTSEVFEWVASKQVQLTIGHEYPLHEAAQALADLQSRKTTGKLLLKCID"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MEVIATAHGGPEVLAVRPSSHTPDATQLEGGQVLVHNAYAGVNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDTYFLSGLYKKPAMPYIVGEEGAGAVVKVGAGVPETMLGKRVAYFGGAGCTGSYAAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVAPASALREVPDGVIDAEAAAVMCQGLIAHYLVDSSYPCGPGSIVVVHAAAGGIGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VCQMAKLRGARVIGVCGGAEKATLARSVGRADVVIDYVATPDWAPLVRAAAPQGVDAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (WIS-NOV-1999) Seattle Biomedical Research Institution, 4 Nickerson Street, Seattle, WA 98109-1651, USA 3 (bases 1 to 41944)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (04-NOV-1998) Seattle Biomedical Research Institution, 4 Nickerson Street, Seattle, WA 98109-1651, USA 2 (bases 1 to 41944)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (24-FEB-2000) Seattle Biomedical Research Institution, 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="predicted using Glimmer, Testcode and CodonUsage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="L6910.13; predicted using Glimmer, Testcode and
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On Feb 24, 2000 this sequence version replaced gi:6425645. Location/Qualifiers
                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
11.5%; Score 18.6; DB 3; Length 37969; llarity 84.0%; Pred. No. 6.7e+02; Conservative 0; Mismatches 4; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nickerson Street, Seattle, WA 98109-1651, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="Quinone Oxidoreductase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Leishmania major"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'protein_id="AAF35929.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:5664"
                                                                                                                                                                    Db 14231 CCCGTCTGGGGGTTCGGCCTCCGGC 14255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="L6910.1"
                                                                                                                   1 cccgtctaggcgttcggtgtccggc 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="Friedlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2880. .3416
/qene="L6910.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /qene="L6910.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'clone="L6910"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                             AC005929.5 GI:7025830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 41944)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CodonUsage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /qene="00R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .41944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leishmania major
                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leishmania.
                                                                                                                                                                                                                                                                                                                                                              sednence.
                                                            21;
                Query Match
                                      Best Local
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                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
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                                                                                                                                                                                                                                                   RESULT
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/protein_id="AAF35930.1"

us-09-899-718a-5.rge

gene

CDS

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AATLLEMTLQTHGLLCGGGVPSQAWSPTPDPADASSGGSSTAALNGTVLLDKFPRLSA
EMLLQHVTYLLSNEAKQRTANAADGAGEGSDS1YLSPQRTRHFGLTGVETLLLSATQA
EQVNQVLPLYVRGHTLPDEVASDITQTRNIHBAVRKTQRVLSRVLQQASQELASQSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YGSVVGIRMLDRAVWEPHYQVAADNKSEAAAATPTAPAAASPSRPSSSSSSSSTASGK
TGIDLVKLSASIQAATWQAIQKVRAAKEETHSRSLRRNPQVLAEARLRDWYEQDANTL
   QQTMSAYARAVMYTEEKQGFEKPVIAVSAEEGTNVPELWEAMLKMWNARLESGQIAHL.
RRAQSTKHFYNYFEMELLAKARRMTNLEMQNMAHRVWEHEMTPREAGDIMVLRTLREH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MLEHRRLFPGRRYDSRVYRSCASPMPYLLEEKLRGTAMEQRTPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEAVISCPATPGLAEGKISAYLLDLATRTLRPPTFPPLSDSTVTAKDTVCLVGGPELA
WLAVGMTPFRNITSVTLQQGELKSCSLQESMEWMRLAHLLKAAPEQVNGDGGEALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRLAAVRTDLVLLDLLANGHPTTGLPQVLATPFADVLDAYVDMEKEQHSAAAPSAPQN
VGRLRSVLFDEEPVTGVHLEQPSLRLRLVSLQQLLVRIVRALSGAHVGLPAGNRPTPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPRPFDGLKNLEATEWMQAVRFGVPQPARYRRPNAAPKDLGEGGDGAHTDQKPRETIT
VLRDEDCDPANIPIGSVHPLFAPGLLQLEVDPNVATNGGSRVDEFFVLSEQRKEMRRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EYAKRMHVHKAILQQAAPLLYYDAWDKSDVHQLDTSCVLVGHFWKAFCALHPRPFHPV
AAPATSGGAGSSQASSTTTTASSSSSSNSNVTSSSSSAGSTPKGAFNPAEWKMAVGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGEGAYLTLSIVQDRVEELLRLATAAYDKHGSTHPELRWLRPKLLVLKGLLTIPLTGH
LLHAQRCIEEAAHYVDALTKRTNLLLDGLKERTHEPELGLYMLLQAEIAARVFDWDVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MSFRYTNHLVATLKHRLFLEAAHRQLVRQTFTGVCNGIEVTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MLRRTLHCCTAVRHTSVPSFMQHPVEMAFYFPRFHPDTHVNAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVVEAQKDNAKSLLLLERGIDILNSVGGVRNPTVANLLRPLYAARFEMLNGSEHLPRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGQVDGDVVNMFTDAAGYYADPPNTTLDGDAIMSERKLAEQRFEVEAYACCLRSYAAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLGASRPEATSTRDSPVFLAKQLFSLNPLLTVATSSSLIFSDVRNVSELPLDMCRRRT
GEALDRALKLNRMLYPDFRQNAPAAATLMTMACMYADTRDYLYATGLFESANKAVTYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTAAVDDAGHNGPHPALAHLPSHLFVRTAGARGPPPGWEYYGVHLGIKAEAMNVRYNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPELIDAVGLMTRHSRSSRAESTASASTSAAESAMSRALPPTRWTTTVSATAQPTTDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NASDTATLHLIDSSGSSNSGGVTATAGSEVGAESTRSGMPG"
17277. .17807
/note="predicted by Testcode and CodonUsage, but no ATG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="predicted using Glimmer, Testcode and CodonUsage; Glimmer predicts start codon at 1887?"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="predicted using Glimmer, Testcode and CodonUsage; Glimmer predicts start codon at 20557"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="predicted using Glimmer, Testcode and CodonUsage;
                                                                                                                                                                              Glimmer, Testcode and CodonUsage; 5' end may extend start codon to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence is not predictive of protein-coding gene"
18721. .19698
/gene="L6910.14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEAFWERVELIRRSQLATIPKGGVKRGYADMADTVQDSIEEKVQLRFTQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FGDTSLEHVFLQKLRYEFLAGVGSEQEAKTASHEVVHLLKRIDALPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Pred. No. 6.7e+02;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAF35935.1"
/db_xref="GI:7025837"
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/db_xref="GI:7025838"
                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAF35934.1"
/db_xref="G1:7025836"
                                                                                                                                                                           /note="predicted using
possible frameshift at
                                                                                                                                                                                                                                                                                                                                                                                   /product="L6910.12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="L6910.14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="L6910.15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 cccgtctaggcgttcggtgtccggc 25
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/gene="L6910.15"
                                                                                                                                                                                                                                                                                                                   /gene="L6910.12"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="L6910.14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="L6910.15"
                                                                       LAADAAVQHDAGKRA"
                                                                                                                                       /qene="L6910.12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24855. .27485
/gene="L6910.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                               15437. .17086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local 3
                                                                                                              gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HRK I EPLESAAGRTAGECMGGWUDTDDPATSSKSLGSFTHACPVAAASRPTFERQQQ
PRRLTAWHWAGRPHLCLNAALRRKAGGNNDRLNYYCREAMHFERSKQGRQYRRQQDEH
PROYDPHLTADRAWNRIEDATGWOGELDDKGCVYCVESHLASLMYTLRDEQRRADAA
TDPWDAASGGASASGROGPPSSVYTMDRLRELGAELQCPYLATRLLIRGADVAFIPY
GYVLDEGQRAVLLGGAATNPATAAEAAAVFATPSRSYPPAAEGGGALQNDVAHSPPSY
GTVLYHRRQRYTATFRRRQQQQDRGGNYYGGDDDDGGEEEAINSTWARRAPPSPSL
GDIFVEDEAHNIADHCRSTSTYTWAPWHILLLARRLETYLARYASRLLTRNKQRLREI
VHFLSKLSGFCRRADSAAVLGEGGGEGDIAPSLSAPSPPLART
LVLPFHTFLFDAGIDSVDVYAFLIFLVUDSQLLMKLQGFVSYALDAELQQERESVSTAM
RTTWTVSGTDSSAGSTAGKRGGGGGGVGVSDAHNEAQRORRLLASLLDDNUHKKRA
                                                                                                                                                                                                                                /note="L6910.2; predicted using Glimmer, Testcode and CodonUsage; ORF starts at 5110, Glimmer predicts start codon at 5110, Testcode and CodonUsage predict start codon
                        /translation="wkilkfynsdaphtladvolknorlwepcrhgnaavaakswtlt
aaspasvsggywlldddsqplceitdvllalpetaanaagssgtfaprgytdkdvdgi
Dfrskmgromereratygatsktatksartmmnaeemtekknermkrereavaeaied
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGEAAPPHLSLAEHLSQQLQPAGVAMTAAAHAGAVAPADPVQLRALTAEALQCVERLL.
CALYVSNTTSTRVLWTPSSLSPTSPARPAGCAVRQGALKVIQLEPGMYTFAPLVLEAR
AVVLAGGTMQPLAFTCGPLLPAQAMVGGDAGGDCGTASTIGRSAVEVAVEGIGGSDYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKELVRQEVEMCAIPGSNIVSAPCLAHTVHMDTLEGITVEETATYEAQANQAAASRDN
EEENPVEHRWVPTAVAQRGYEAAFTLSITRNATVHYLTFYLDAAFTSKTNPGANFVLA
VRPGGENNWTEVSVGLREPLPVNVGEKIQGTLRIYTPADKGGKITVVEVTAKTEGQVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MMSRVPRPHIHQRISVEDIMKGNRRTLARAITLAESSNPADSTR
LGNLLREIHQMATVRTVPRFALSGSPGSGKSSLLDTLGYYLCEKKNMHVGVLAVDPSS
TITHGSILGDKTRMEKLGTHLNSYIRPSPSGGHLGGVTSRAWEALEIFEAARFDVVFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HCIDASLQGGVAPAPGPSAFHLISEGHVVPSSSYQVWALGIGPSGLRMELSQQALGLR
SNAASTSNDTGSSRIGVSSIISPHAHRVLAEVGCTLLNLARVLPPAGAICFFTSYDVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HDSEKAALDYSPPSPTLDEVLRQRQLEEEMVQVRRERRARVRAQRRQIRQARKLMRLO
QQLTNSGGEHDFLLTQDPLAMYAEQLSMKKARLRGDDLVDLHSASSLSSSSSSSSSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLSEGINFADDLGRAVVVLGMPYANPTDVEMRMNLKHIVATRLRANADADRRGMRGTA
GSASTPSPASSSPFTCAEEWGLYMDSMMRTVNQCIGRCIRHAGDYATIILLDARYTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MLLNSILSYLFDPVEDAKDVDGTASGSGSSVVAEPPAAMATAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAREDDDDAEAQLEAALSTLIPLRKPKVYFASRTHTQLQQLMEDLQRTAFARLPLRPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="L6910.10; predicted using Glimmer, Testcode and CodonUsage"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Blastp similarity to CHL1 helicase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="Helicase 1"
/protein_id="AAF35931.1"
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/db_xref="G1:7025834"
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/gene="L6910.11"
/note="predicted using
12821. .13870
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'db_xref="GI:7025832"
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                                                                                                                                    NDASVMEPRKKERKHSKK"
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/gene="L6910.11"
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/gene="PAMT"
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/gene="HEL1"
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/gene="HEL1
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/translation="MKLVPVALLYLGSLAFLGADFARLDVASEFRKWNKWAVSRGKR
ELRVSSSYPTGLAEVKAGPAQTLIRTQDVKGASRNPQTSGPDAARIRVKRYRQSMNNF
QGPRSFGCRFGTCTVQKLAHQIYQFTDNDKDGVAPRSKISPQGYGRRRRRSLPEPGLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The mycarose-biosynthetic genes of Streptomyces fradiae, producer
                                                                                                                                                                               Submitted (02-FEB-1998) Molecular Cytogenetics, Mayo Clinic and Foundation, 200 First Street, SW, Rochester, MN 55905, USA 4 (bases 1 to 1466)
                                                                                                                                                                                                                                                                                          Submitted (19-JAN-1999) Molecular Cytogenetics, Mayo Clinic and Foundation, 200 First Street, SW, Rochester, MN 55905, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (30-APR-1999) Biochemistry, University Of Leicester,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                         Sequence update by submitter
On Jan 20, 1999 this sequence version replaced gi:3372495.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 70.0%; Score 18.2; DB 4; Length 1466; Best Local Similarity 87.0%; Pred. No. 1.1e+03; Matches 20; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bate, N., Butler, A.R., Smith, I.P. and Cundliffe, E.
                                                          Cloning of cDNA encoding canine adrenomedullin Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="adrenomedullin precursor"
/protein_id="AAD05423.1"
/db_xref="GI:4164450"
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Location/Qualifiers
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                                                 Imoto, I. and Jougasaki, M.
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Direct Submission
                                                                                                                                                                                                                                                and Jougasaki, M.
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ELRVSSSYPTGLAEVKAGPAQTLIRTQDVKGASRNPQTSGPDAARIRVKRYRQSMNNF
QGPRSFGCRFGTCTVQKLAHQIYQFTDKDKDGVAPRSKISPQGYGRRRRRSLPEPGLR
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                                                                                                                                         MAM 28-JAN-1999
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Jougasaki,M., Schirger,J.A., Simari,R.D. and Burnett,J.C. Jr.
Autocrine role for the endothelin-B receptor in the secretion of
                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                          cDNA cloning of canine adrenomedullin and its gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="encodes proadrenomedullin N-terminal 20 peptide"
                                                                                                                                       CFU96127 1432 bp mRNA linear MAM 28-JAN Canis familiaris adrenomedullin precursor, mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ono,Y., Kojima,M., Okada,K. and Kangawa,K.
Direct Submission
Submitted (02-APR-1997) Biochemistry, National Cardiovascular
Center, Pujishirodai 5-7-1, Suita, Osaka 565, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.0%; Score 18.2; DB 4; Length 1432; 87.0%; Pred. No. 1.1e+03;
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/protein_id="AAD09957.1"
                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 1432)
Ono,Y., Kojima,M., Okada,K. and Kangawa,K.
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426 c 401 g 299
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                         Db 38425 cccercreegeerreegecreege 38449
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VILQYCGIGERDLPCIGEVSPEKAGRFTPGTGIPIVSEEDAKAMRPDQLLVLPWIYRE
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RHVIRSCEASLRRLGVDHIDLYQMHRWDRTVRWDELMQAMDQLVASGRVRYIGSSNFA
GWHLAAGQESAARRGSLGLVSEQCLYNLAVRRAELEVLEAARRYGIGYPAWSPLHGGL
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GVSGAVIGPRTTGHLVSALRAVELELSEEEHRELEALFPPVGSGGEVPEAWQN"
complement(1066. .2109)
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RDLLDVRDAATAFTTALEHADOLRGKHWVVGTGRRHRLDRVFGTVAALAAEHTGRPPV
PVVTVDPPGYAEVCDFRTPDSDPSAFRAVTGWRPRAEPADGIAAAIAAVAGAGDSPEP
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AYDIVCHEHLEYYALQQIEWMAERAGLTVLRAELTDVYGGSLCVTLARASSPHPRDEA
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                                                                                                                                                             /function-"biosynthesis of NDP-mycarose during tylosin
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/function="biosynthesis of NDP-mycarose during tylosin
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/protein_id="AaD41824.1"
/db_xref="G1:5305794"
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                       complement(80. .1069)
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/db_xref="taxon:1906"
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/note="orf8*"
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/gene="tylcv"
/note="orf7*"
3575. .4960
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/gene="tylcv"
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ABC transporter permease; ABC transporter, ATP-binding component; bldA regulation: cytobrome P450; hydrolase; integral membrane protein; LacI-family transcriptional regulatory protein; prolyl aminopeptidase; RNA polymerase sigma factor; ROK (NagC/XyLR) family transcriptional regulator; secreted solute-binding lipoprotein; TetR-family transcriptional regulatory protein; TTA codon. Streptomyces coelicolor A3(2)

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycesols: Streptomycetaceae; Streptomycesols: Streptomycesols: Streptomyceneogicals: Streptomyceneogicals: Streptomyceneogicals: Streptomyceneogicals: Streptomyceneogicals: Streptomycesols: St
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QDASGSVAVYLDPGGLGYVALADDTCMNYLYTREYTPGMIIDIDALDPGLGLFWNLT
EPPVRSERDAAAPSLAEAAAGTLPGYEQCLRAYPAM"
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                                                                                                                 IELTARAEKLLKEHGTTSDPVAFAATVQSGPGLFYMPRYFQYAGETFDDRHHFVGPCA
PRASFHGTWQRPEDGRPLVMVSLGTIYNERPGIFRACVEAFRDRPWNILLVLGGGLGA
                                                                                                                                                                                        GDLGPLPENVLVRDFVPLGDVLPHTDLLVNHGGTSTAMEALAHGVPIVAMPEMPEPRA
TARRIAELDLGDWLLPGEVTAEKLSGIAQRVLTDDRIRKGLDRMRGEIRRAGGPAVAA
                                     RVGARAVTYPLDRERFRADMVPKEESDEYTDEGEFLKVLEWLLDTTADTLPLLESAFA
                                                                           EDRPDVVANDPSTFWTGLLLAGKWDIPVIRSTPSYASNEHWALHPPFEPGAAQVDPAL
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GRFRRAPDEGSCRMAHIAFFILPAAGHVNPTLGVAEELAARGHRVTYALPEDMADRAV
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Thomson, N.R., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
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                                                                                                                                                                                                                                                                           /gene="tylcvi"
/note="ori6*"
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SCF43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
JOURNAL
REFERENCE
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JOURNAL
                                                                                                                                                                                                                                                                                                                     gene
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VERSION
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Streptomyces coelicolor sequencing at The Sanger Centre is funded

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Contains possible membrane spanning hydrophobic domains."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical protein SCF43.03."
/protein_id="CaB66192.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(2947. .3255)
/gene="SCF43.04c"
/note="SCF43.04c, unknown, len: 102 aa."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAB66194.1"
/db_xref="GI:6714729"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(2947. .3255)
/gene="SCF43.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="GI:6714728"
                                                                                                                                                                                             /db_xref="GI:6714726"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="GI:6714727"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="SCF43.03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SCF43.03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
                                                                                 /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPMRGRKVG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="SCF43.02"
//note="SCF43.02, possible integral membrane protein, len:
379 aa. Almost identical to Streptomyces lividans
TR:P72466(EMBL:270724) substrate hyphae associated
protein, Orf3 (329 aa), fasta scores opt: 2115 z-score:
2334.5 E():0 99.4% identity in 329 aa overlap. Also weakly
similar to Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phosphatase (231 aa), fasta scores opt: 186 z-score: 245.7 E(): 2.6e-06 41.9% identity in 86 aa overlap."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="IDADDAIEATASADDVDAGKPAPEPVEHALELAGVPAERAVFVG
DTVWDMRAGSRAGVRCYGVLCGGLPRADLEEAGAEAVYADPADLLASLRGSPLA"
                                                                                                                                                                                                                                                                                                                                                                                                                       CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SW:YOBU_MYCTUTEMBL:277724) hypothetical 36.8 KD protein (355 aa), fastea scores opt: 208 z-score: 236.0 E(): 9.38-06 26.18 identity in 303 aa overlap and to a downstream CDS, SCF43.07, putative integral membrane protein (419 aa), fastea scores opt: 276 z-score: 252.1 E(): 1.28-06 28.18 identity in 366 aa overlap. Note SCF43.02 is 50 aa longer than Streptomyces lividans Orf3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="SCF43.01"
/note="SCF43.01, possible hydrolase, partial CDS, len: > 98 aa. Identical over the available sequence to Streptomyces lividans TR:P72465(EMBL:270724) substrate hyphae associated protein, Orf2 (218 aa), fasta scores opt: 648 z-score: 826.2 E(): 0 100.0% identity in 98 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.nih.go.jp/
jun/cqi-bin/frameplot.pl. CAUTION: We may not have predicted the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            correct initiation codon. Where possible we choose an initiation
                                                                                                                (URL; http://www.sanger.ac.uk/Projects/S.coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S.coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                   The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS. Usually the highest scoring match found by fasta o is given for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        overlap. Also similar to several phosphatases e.g. Streptomyces collinus TR:09X654(EMBL:AF131877) NapH
           by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are
available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMPORTANT: This sequence MAY NOT be the entire insert of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Streptomyces coelicolor A3(2)"
/strain="A3(2)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAB66190.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:100226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              xref="GI:6714725"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="cosmid F43"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "SCF43.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dene=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cosmid F43
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Source

FEATURES

gene CDS gene

CDS

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overlap. Also highly similar to Streptomyces coelicolor TR:087855(EMEL:AL031013) putative transcriptional regulator SC8A6.21c (441 aa), fasta scores opt: 2034 z-score: 2241.7 E():0 71.4% identity in 434 aa overlap. Contains a Pfam match to entry PF00480 ROK, ROK family and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EAVAAAGVPALVHASSYGAYSPCPKNHAVDESWPTHGWPDAAYCREKAYLERÄLDTFE
RDHPGIRVVRMRPAFLFKRESASEQRRIFGGRFLPGPAARPELLPFLPDVPGLRVQAL
HTDDAARAYRLAVRSADARGAFNLAAEPPVDAELLGELLGVRPVRLPRAAARSAIAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="SCF43.03, unknown, len: 343 aa. Almost identical to
Streptomyces lividans TR:P72467(EMBL:270724) substrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MSSATGSKIVVTGATGNVGTSVVRLLSEDPEVGTVLGLARRIPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MSDHRHEGPGENCAPVPRDMPDQQAGDHDDPWEAASPTREQSEH
RQGPDGERPVDDAESAGDAETGPVPDVPDTDEAGTGRQGAPHSAAVHPEHPVPDESSG
                                                                                                                                                                                                                                                                                                                         VWLGDPMALMAPWVALVLVQATVYSSVRQAGQQFAAICTGALLASAAQAIMDDNTGAL
                                                                                                                                                                                                                                                                                                                                                                                                                    VLSLPVLMLVANWSRFGGQGIYAATTAVFVLASGTAVSAAAVGHRMGQAALGAVIGVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VNALVLPPIHLRDVRENLAALAREAGDLLHSVAADLRETQWDAQSAAGWTSDAARLER
RLEALYSARSWSRESLRLTSGRLRRLHRAPTVVPPEDEDERKWSRVTGNLGALTRTLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AADEHRTPAPPEGPVLDLYARLLRLIGDACHTEAGRWAGERPGADPATATEETMEELH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WSPAKTEWAAVDLASEQSDLTSHFADADAVVHLAWAFQPTHDPATTWRTNVLGSIRVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WGMRLLPASPHLFDAVLRLPVMDCTRARVELGWGATRTATEVLEEFLRGLRQGAGADT
                                                                                                                                                                                                                                               /trans.lation="MWWEACAVGRAVRAAWRGPGRERDLVVQSLKAAGAALIAWTVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative ROK (NagC/XyLR) family transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hyphae associated protein, Orf4 (343 aa), fasta scores opt: 2274 z-score: 2584.7 E():0 99.1% identity in 343 aa overlap. Also weakly similar to Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TR:09WX08(EMBL:AL079345) putative epimerase (353 aa), fasta scores opt: 275 z-score: 318.0 E(): 2.5e-10 25.9% identity in 340 aa overlap."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(3320. .4609)

Agene="SCF43.05c"

Complement(3320. .4609)

/gene="SCF43.05c"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         xylose repressor (399 aa), fasta scores opt: 51
z-score: 575.9 E(): 1.1e-24 28.1% identity in 402
/product="putative integral membrane protein." /protein_id="CAB66191.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRLQEGLREHAGQGAARTAVLGTLLLQAENLWAEIVPEPRESAEQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical protein SCF43.04c." /protein_id="CAB66193.1"
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4799. .5293
/gene="SCF43.06"
/note="SCF43.06, unknown, len: 164 aa. Highly similar to a
                     SYSNVVADLVADGLVEEAGSVDSDGGRPRTLIRVAPASGHMIGVDVGETRVRVEIFDL
THELEARABERLARQHEDVVIVGHVROSIARLARAGLPBERLLGGGIGVPGTYBHT
ADRGAVVHGOTIGMANYPLEALLARGSPLPDTVPCI.IDNGARTLGGAEMWFGAGRGAR
NAVVLLFGSGVGASLVTPEAEQGRAVEWGHLTVRVRGRRCRCGGLGGLEAYAGRSLL
NAVVEREBGGRYVPEGTDBETALTAMLAAAYPADGAAADPVALAVLEETABEYLGAGLSDLI
NLEOPERILIGGWAGLQGARRIAAAYAAYBAGAADPVALAVLEETABEYLGAGLSDLI
ALLPLADFFRAGGRRPEPANRRHANSYALRHPARKVTVDLGRLGPDAVTVGA
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translation="MAGRNGRTVRDLRRANRTAVLQRLYFDGPLSRFELGPATGLSSG"
                                                                                                                                                                                                 complement(3785. .4033)
/gene="SCF43.05c"
/note="Pfam match to entry PF00480 ROK, ROK family, score 22.80, E-value 1e-05"
complement(4614. .4618)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 173434)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein of unknown function from Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaul.R.K., Olson.M.V., Raymond,C. and Haugen,E.D.
Direct Submission
Submitted (06-NOV-2001) Genome Center, University of Washington,
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Sequencing vector: plasmid; L08752; 68% of reads
Chemistry: Dye-terminator E1; 89% of reads
Chemistry: Dye-terminator B10 Dye; 11% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 170284 bases at least Q40
Consensus quality: 172588 bases at least Q30
Consensus quality: wum-of-contigs
Linsert size: 172934; sum-of-contigs
Quality coverage: 8.7x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN
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On Nov 6, 2001 this sequence version replaced gi:13157584
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.0%; Score 18.2; DB 1; Length 22396; 87.0%; Pred. No. 1e+03; 1ve 0; Mismatches 3; Indels 0;
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Direct Submission
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Contact: uwgchtgs@u.washington.edu
Drafting Center: SC
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Center clone name: RP11-480112 (sc0719)
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4799. .5293
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Direct Submission
Submitted (15-FEB-1996) W. Piepersberg, Bergische Univ.
Gesamthochschule, Wuppertal, Institut fuer Chemische Mikrobiologie,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang,H.Z. and Piepersberg,W. Cloning and characterization of the mel-operon from S.lincolnensis
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Zhang, H.Z. and Piepersberg, W.
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mel-operon; melCl gene; melC2 gene; ORF3; RNase H; rnhH gene;
tyrosinase; tyrosinase co-factor.
NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Pred. No. 9.4e+02;
0; Mismatches 3; Indels 0;
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Streptomyces lincolnensis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                  9114: contig of 9114 bp in length 9214: gap of unknown length 27205: contig of 17991 bp in length 27305: gap of unknown length 47551: contig of 20346 bp in length 47751: gap of unknown length 74121: contig of 26370 bp in length 112038: contig of 37817 bp in length 112138: gap of unknown length 112138: gap of unknown length 112138: contig of 51296 bp in length 173434: contig of 61296 bp in length
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S.lincolnensis melCl, melC2, ORF3 and rnhH genes.
X95703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="RPI1-480112"
/clone_lib="RPCI human BAC library 11"
1. .9114
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/note="assembly_name:Contigl13"
27306. .47651
/note="assembly_name:Contigl14"
47752. .74121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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87.0%;
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Best Local Similarity 87.0
Matches 20; Conservative
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                   6927 bp
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/db_xref="G1:12082816"
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Chang, Z. and Vining, L.C.
Direct Submission
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                                                                                                                                     Streptomyces venezuelae.
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                                                                                              AF319543.1 GI:12082814
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/qene="CbsSV"
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/qene="CbsSV"
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/db_xref="SWISS-PROT:P55049"
/db_xref="SWISS-PROT:P55049"
/translation="MSYVPESIEVGYPVHTAYNQWTQFETFPQFMSGVERIEQRTDTL
THWWTSVNGYTEPABLTEQIPDERYAWTTVGGRAEQAGVYTFHKLDDDHTKVMLQM
DFHPDSVTEKVGDKLGFVKRQTKGDLERFKKFIEERGQETGGWRGAVI"
                                                                                                                                                                                                                                                                                   /db_xref="SWLSS-PROT:P55048"
/translation="MPRLTRRRALTAAAALASGAGAGAGAGAAAAAPGAAAHDHGSPDV
PLPCSLLDLLPLLLLDEVIKGRGIQGGPHRGGGHHHGTGYAVFLDGVELHVMRNAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGGTGRSRNGRVTDGPFRAATGVWPITVRLDGRTYLRRALGGAGRELPTRAEVDSVLS
IPTYDMAPWNSASDGFRNHLEGWRGVNLHNRVHVWVGGQMATGVSPNDPVFWLHHAYI
DKLWAQWQRRHRTPAYVPAAGTPDVVDLDETWKPWHDSSPADLLDHTGHYTFDTD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MTVRKNQATLTADEKRRFVTAVLSSSAARVDTFVTTHNEFIVAD
TDNGERTGHRSPSFLFWHRRFLLEFERALQSVDASVALPYWDWSTDRSARSSLWAPDF
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TNNVAELTALERLLAATDRDVPLEIRMDSQYAMKAVTTWLPGWKRNGWKTAAGKPVAN
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                                                                                                                                                                                                                                /product="Tyrosinase co-factor (MelC2)"
                                                                                                                                                                                                                                                                                                                                            GSWISVVSHYDPVPTPRAARAAVDELQGAKLVPFPAN"
                                                       /organism="Streptomyces lincolnensis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="SWISS-PROT:P55023"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             458 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="SPTREMBL:Q54388"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="putative RNaseH"
Gaussstr. 20, 42097 Wuppertal, FRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="CAA65000.1"
/db_xref="GI:1200140"
                                                                                                                                                                                                                                              /protein_id="CAA64999.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAA65001.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAA65002.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(2204. .2557)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(2204. .2557)
                                                                                            /db_xref="taxon:1915"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="Tyrosinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="GI:1200142
                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                          /strain="78-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="ORF3"
1369. .1821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                             /gene="melC2"
465. .1286
                                                                                                                                 /gene="melC1"
                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="melC2"
                                                                                                                                                                       /gene="melC1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="ORF3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="rnhH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="rnhH'
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                   FEATURES
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RESULT 13

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BCT 11-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDPRDIDDLMLGCGLPGGGQGNNLGRIVAVQMCMDHLPGCTIHRYCSSSLQTSRMALH
AIRAGEGDVFISAGVEMYSRFVKGNSDSLPDTHNPLFADAEARTAAVAASEGSSWHDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REDGLVPDAYIAMGQTAENLARWKGITRQEMDEFGYRSQNLAEQAIKNGFWEREITPV
TLPDGTVVSTDDGPRAGVTLEGVSGLKPVFRPDGLVTAGNCCPLNHGAAALVIMSDTK
ARELGLTPLARIVSTGVSGLSPEIMGLGPVEASKQALQRAGLTIGDIDLAEINEAFAA
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/db_xref="GI:12082815"
/translation="MQFHDSMISLVGNTPLVKLNNVTAGIQATVLAKVEYFNPGGSVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DRIAVRMIEAAEQSGELKPGGTIVEPTSGNTGVGLAIVAQQKGYKCIFVCPDKVSLDK
INVLRAYGAEVVVCPTAVDPEHPDSYYNVSDRLVRETPGAWKPDQYSNPNNPRSHYET
TGPELWEQTDGKITHFVAGVGTGGTISGTGNYLKEASGGSVKIIGADPEGSVYSGGSG
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ALEVARELGPDDVVVVLLPDSGRGYMGKIFSDEWMAGHGFLEDTSSATVADVLRHKEG
GTMPSLVHMHPDETVGQAIEVLREYGVSQMPIVKPGAGHPDVMAAEVVGSVVERDVLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cystathionine beta synthase in Streptomyces venezuelae ISP5230: an alternative pathway of cysteine biosynthesis Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (05-NOV-2000) Biology, Dalhousie University, Halifax, NS
                                                                                                                                                                                                                                                                                                                                                                                             Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                           Streptomyces venezuelae putative acetyl-CoA acetyltransferase and cystathionine beta-synthase (CbsSV) genes, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function="catalyses the formation of cystathionine from homocysteine and serine" \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                venezuelae ISP5230: cloning, sequencing, functional analysis and relevance to chloramphenicol biosynthesis
Thesis (1999) Dalhousie University, Biology, Halifax, NS, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genes for cysteine biosynthesis and metabolism in Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative acetyl-CoA acetyltransferase"
                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18; DB 1; Length 6927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.2%;
80.8%;
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Matches

DEFINITION

ACCESSION

RESULT 14 AC109873

ORGANISM

KEYWORDS

SOURCE

VERSION

REFERENCE AUTHORS

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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* consists of 12 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                             Quality coverage: 0.1x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INV 20-MAR-2001
                                                                                                            Sequencing vector: Plasmid; M77789
Sequencing vector: Plasmid; M77789
Assembly program: Phrap; version 0.990329
Consensus quality: 22789 bases at least 040
Consensus quality: 25322 bases at least 040
Consensus quality: 2555 bases at least 030
Consensus quality: 2755 bases at least 030
Consensus quality: 2755 bases at least 030
Estimated insert size: 16593; sum-of-contigs estimation outlity coverage: 0x in 020 bases; agarose-fp estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conserved WD40 repeat domain protein; kinesin-related protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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AL049768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3510: gap of unknown length
4516: contig of 1006 bp in length
4616: gap of unknown length
6190: contig of 1574 bp in length
6290: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1524: contig of 1524 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gap of unknown length contig of 1786 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig of 2447 bp in length
gap of unknown length
contig of 2021 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of 2021 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bp in length.
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unknown len
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                                                                                               clone name: CH230-303015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap of unknown
contig of 2253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
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gap of unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig of 1534
gap of unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gap of unknown contig of 1431
                     Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10116"
/clone="CH230-303015"
4570 c 4492 q 53
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                                                                    Center project name: GQIO
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gap of
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10958:
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                                                                                            Center
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
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RATURE
                                                                                                                                                                                                                           AC109873 20633 bp DNA linear HTG 08-FEB-2002
Rattus norvegicus clone CH230-303015, *** SEQUENCING IN PROGRESS
               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (08-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
             Gaps
          ;
0
       5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Baylor College of Medicine
  0; Mismatches
                                               12 unordered pieces.
                                                                                                                                                                                                                                                                                                                                AC109873.1 GI:18640591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 20633)
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21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                           HTG; HTGS_PHASE1.
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Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                Norway rat
                                                                                                                                                                                                                         AC109873
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JOURNAL AUTHORS REFERENCE

TITLE

JOURNAL

COMMENT

ORGANISM

REFERENCE AUTHORS 98146435

JOURNAL MEDI, I NE REFERENCE

TITLE

JOURNAL

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AUTHORS

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/note="Pfam match to entry PF00400 WD40, WD domain, G-beta
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Trypanosoma brucei TREU927 sheared genomic DNA Trypanosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="Spprembl.gonp84"
/db_xref="Spprembl.gonp84"
/translation="MPPTSLTSRSSPPVATAAPRPVGAORRPSKEVQELIDKRTEEL
KOETCOHEKKFIGGRWYDDTAALRNRGTRRREELNRAPKRLAKVDMYYGMEDNTGL
LLDDHEKADRIGSGPRIAGSGPVDLOTOOKRYSTVLDKLGPYKIDFSINGTHLLLAGLRGH
MANITRWKSFQLEGETQLKDRISDAIFLVDHSWTAVAQKKFVYMYTKEGTEMHLLSKMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVGRDEEVDEELĞYKEAPKTKEVKSRQELQRERKMAKWDKKDSADKVRSKQTLRASRI
VQRNRAQWARDARNGVFDENALDAEETEALAAASRAAKQHKKLARKEALEIANDIRGQ
LRQDVDYDLEVPPAQRRRFEKSYHGSDTAGRGTEGRGSSGPEAEARTNAALKRFLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="pfam match to entry PF00400 WD40, WD domain, G-beta
repeat, score 25.60, E-value 0.0012"
                                                                                                                                                                                                                                                                                             /note="poly-pyrimidine tract"
complement(1314. .1707)
/note="region of BLASTW similarity to: AF139112 Leishmania
peruviana clone Ac16 microsatellite sequence., bases
1. .394, 83% identity over 393 bases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HMDRLGYLEKHMILAATSSTYSTMQYLDISTGQEVGTKVPAVMRDPTSCLAVNPSNGV
AATCDLRGVVKFWSPTVVDPLLQLKGHKGVIEDICFHPNGRFFLTLGGDHAMKVWDCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLRTLEEYAVTYSFHTLDISSSGLVALGGGTNVHIWKDMFTAAKPSSPYMKFGLGYGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IAEQVRFCPFEDVIGIGHSRGFTSLLIPGSGEANPDFYYANPHETERHRKERVVTNLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKLPPDTISMDIQVPGVNEKRLAEYNENLRLNRKARAIREKKMRRASKSLGEAAPTGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYTIP (LYTI) gene; contains two Pfam matches to entry PF00400 WD40, WD domain, G-beta repeat; reasonable similarity to 99787, conserved hypothetical protein (554 aa, Neurospora crassa, EMBL: AL355932, CAB91444); Fasta scores: E():0, 34.9% identity in 502 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trypanosoma cruzi LYT1p (LYT1) gene, LYT1-a allele,
complete cds., bases 4054. 4922, 66% identity over 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Irypanosoma cruzi LYT1p (LYT1) gene, LYT1-a allele, complete cds., bases 4974. .5751, 71% identity over 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        590-610; good similarity to AF253317 Trypanosoma cruzi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="region of BLASTN similarity to: AQ644878
RPC193-DpnI:-25G1.TV RPC193-DpnII Trypanosoma brucei
genomic clone RPC193-DpnII-25G1, bases 1. .608, 678
identity over 607 bases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="L6586.01, len = 679 aa, conserved hypothetical
protein; predicted pI = 9.8667; predicted coiled-coil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="region of BLASTN similarity to: AF253317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="conserved WD40 repeat domain protein"
/protein_id="CAB71230.1"
/db_xref="GI:6855407"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="region of BLASTN similarity to: AF253317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat, score 7.00, E-value 66"
                                                                                                                                      /note="(gcgtgt)3"
488. .512
/note="poly-pyrimidine tract"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(1578. .2185)
/db_xref="taxon:5664"
                                                                       /clone="cosmid L6586"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="L6586.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="L6586.01"
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/gene="L6586.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1424. .2292
/gene="L6586.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'qene="L6586.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'qene="L6586.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="L6586.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=L6586.01
                                           /chromosome="23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region at aa
                                                                                                              .170
                                                                                                                      repeat_region
                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                         repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid L6586 is not overlapped by any clones sequenced to date. It contains the left end of PAC P460 (AL160762), and the right end of PAC P986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Where possible we choose an initiation codon (atg) which is preceded by a stretch of pyrimidines or part of a Kozak sequence. If this cannot be identified we choose the most upstream initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the Hexamer program which was written by Richard Durbin as an integral part of the ACEDB-based analysis tools for the C.elegans Genome Sequencing Project. The program calculates the log-likelihood score for a given DNA segment based on the frequency of 6-mers, normalised for the base-pair composition of the genome. The program was trained using a fasta file of confirmed Leismania major coding sequences (CDS), i.e. from ATG start codon to the stop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS are numbered using the following system eg L6586.01. L6586 (cosmid name), .01 (first CDS)

To make the cosmid library Leishmania major Friedlin DNA was partially digested with Sau3Ar prior to cloning into BamHI site of the cosmid shuttle vector cLMTG (Ryan et al. 1993 Gene 131:145-150). The sequence of the packaged vector was determined by Peter Myler and Ken Stuart at Seattle Biomedical Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Details of leishmania sequencing at the Sanger Centre are available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in codons is given for each CDS.
Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-MAR-2001) European Leishmania major Friedlin genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, (E-mail: barrell@sanger.ac.uk) and Max Planck Institut fuer Molekulare Genetik, Ihnestr. 73,
                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 40064)
Klages,S., Borzym,K., Reinhardt,R., Beck,A., Ivens,A.C., Quail,M.,
Rajandream,M.A. and Barrell,B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Institute, and is available as accession number U59231. The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAUTION: We may not have predicted the correct initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon. Transmembrane domains were predicted as implemented at the TMHMM server: http://www.cbs.dtu.dk/services/TMHMM-1.0/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           jun/cgi-bin/frameplot.pl. (2)
codon preference based on the codon usage table for Leishmania at
                                                                                                                                                                                                                             Ivens, A.C., Lewis, S.M., Bagherzadeh, A., Zhang, L., Chan, H.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D-14195 Berlin, Germany
On Feb 2, 2000 this sequence version replaced gi:4760361.
see http://www.ebi.ac.uk/parasites/leish.html
                                                                                                                      Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                             A physical map of the Leishmania major Friedlin genome Genome Res. 8 (2), 135-145 (1998)
           transmembrane protein; ubiquitin activating enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  see http://www.sanger.ac.uk/Projects/L_major/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Leishmania major"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the FramePlot program of Bibb et al., Gene 30:157-166(1984) as implemented at http://www.nih.go.jp/
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/strain="Friedlin"

source

FEATURES

us-09-899-718a-5.rge

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brucei genomic clone 292d02 forward, bases 1. .434, 67%

1352. .5542

/note="poly-pyrimidine tract"
/note="poly-pyrimidine tract"

3908. .3926. .4010
/note="poly-pyrimidine tract"

3905. .4010
/note="poly-pyrimidine tract"

0.0001=0.001y pyrimidine tract"

0.0001=0.01y pyrimidine tract"
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/note="(gct)4"

8687. .8628

/note="poly-pyrimidine tract"

8845. .8862

/note="poly-pyrimidine tract"

882. .8914

/note="poly-pyrimidine tract"

9523. .9539

/note="poly-pyrimidine tract"

9521. .9969
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Search completed: July 31, 2002, 14:01:53 Job time: 17555 sec

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(without alignments)
107.049 Million cell updates/sec
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                             383533 segs, 122816752 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                    - nucleic search, using sw model
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72
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 37, Appl Sequence 79, Appl	1, 1	26, 1	Sequence 1, Appli Sequence 30, Appl	80,	80,	21,	22, 1046	61,	Sequence 3, Appii Sequence 7, Appli	m u	Sequence 251, App	99,	134,	134,	
SUMMARIES	US-08-883-795A-37 US-08-781-891-79	PCT-US95-06815-1 US-08-706-037-26	US-09-005-397-26 US-08-903-800A-5 US-09-036-987A-1	US-09-370-700-1 US-09-232-191-30	-09-23	US-09-232-201-80	-08-724-394A -08-724-394A	US-08-724-394A-22 US-08-998-416-1046	-09-315-793-	9-386-80-	US-08-551-459-3	-09-042-353	US-08-758-417A-99	-053-13	US-08-645-641-134	-08-096-762-
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US-08-308-865-134 PCT-US92-10983-134 US-07-78-890A-1 US-08-814-052-19 US-08-814-052-18 US-08-814-052-18 US-08-939-218A-1 US-08-940-661A-1 US-08-940-61A-1 US-08-448-938-9 US-08-453-924-2 US-08-453-924-2 US-08-471-791-29 US-08-471-791-29 US-08-308-66 US-08-308-68-66 US-08-308-68-66 US-08-308-68-66 US-08-308-68-66 US-08-308-68-66 US-08-308-83-66	US-U8-409-88U-0
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228 828 83 83 83 83 83 83 83 83 83 83 83 83 83	45
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ALIGNMENTS

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Awang, Greevieve
APPLICANT: Awang, Greegor
TITLE OF INVENTION: Recombinant DNA Molecules and Expression
TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
NUMBER OF SEQUENCES:
ADDRESSE: BERESKIN & PARR
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/883,795A
FILING DATE: 27-JUN-1997
CLASSIPICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Gravelle, Micheline
REGISTATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7841-062
                                    ; Sequence 37, Application US/08883795A ; Patent No. 5985607
                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 2529 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                      ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; IMMEDIATE SOURCE:
; CLONE: Rh 10
US-08-883-795A-37
                                                                                                                                                                                                                                                                                     STATE: Ontario
COUNTRY: Canada
ZIP: MSH 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA ORIGINAL SOURCE:
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RESULT 1
US-08-883-795A-37
                                                                                                                                                                                                                                                                    CITY: TOR
STATE: OR
COUNTRY:
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Gaps ö 33.1%; Score 23.8; DB 2; Length 2529; 59.7%; Pred. No. 2.3; tive 0; Mismatches 27; Indels 0 Query Match 33.1 Best Local Similarity 59.7 Matches 40; Conservative

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CORRESPONDENCE ADDRESS
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; LOCATION:
PCT-US95-06815-1
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           Gaps
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                                                                                                                                                                            RESULT 2
US-08-781-891-79/C
US-08-781-891-79/C
Sequence 79, Application US/08781891
Patent No. 6090620
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Mulligan, John T.
APPLICANT: Goffellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 tcggtgccttaagacacctacctttgtgtctatgacatgtgagcccaacagt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA

ZIP: 98104-7092
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC 1996
CLASSIFICATION: 8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/ACENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION WINBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application PC/TUS9506815 GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (206) 622-4900
TELEPRAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 87350 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 32.28
Best Local Similarity 65.49
Matches 34; Conservative
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TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Washington
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US-08-781-891-79
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                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06815
FILING DATE: 31-May-1995
ADDRESSEE: Novo Nordisk of North America, Inc. STREET: 405 Lexington Avenue, Suite 6400 COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                     NAME: LOWINGY, KAITEN A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4184.204-WO
TELECOMMUNICATION INFORMATION:
TELECHONE: 212 867 0123
TELEFAX: 212 867 0123
TELEFAX: 212 867 0124
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3187 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Myceliophthora thermophila
                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/253,781
FILING DATE: 03-June-1994
ATTORNEY AGENT INFORMATION:
NAME: LOwney, Karen A.
                                                                   ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
US-08-706-037-26
US-08-706-037-26
; Sequence 26, Application US/08706037
; Patent No. 5770419
; GENERAL INFORMATION:
; APPLICANT: Xu, Feng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1261...1332
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Best Local Similarity
Matches 35; Conserv
                                               RY: U.S.A.
10174-6401
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CITY: I
STATE:
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APPLICANT: Berka, Randy M.

APPLICANT: Wahleithner, Jill A.

TITLE OF INVENTION: BLUE COPPER OXIDASE MUTANTS WITH

TITLE OF INVENTION: BNHANCED ACTIVITY

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 57704190 No. 5770419disk of No. 5770419th America, Inc.

STREET: 405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 getteggtgeettaagacacetacetttgtgtetatgacatgtgageecaacagt 69
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; LOCATION: 1338..2309, 2457..2525, 2619..3029)
US-08-706-037-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 31.9%; Score 23; DB 1; Length 3192; Best Local Similarity 63.6%; Pred. No. 5.2; Matches 35; Conservative 0; Mismatches 20; Indels
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Patent No. 5972670

GENERAL INFORMATION

APPLICANT: Xu, Feng
APPLICANT: Berka, Randy M.

APPLICANT: Wahleithner, Jill A.

TITLE OF INVENTION: BLUE COPPER OXIDASE MUTANTS WITH
                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,037
FILING DATE: 30-ANG-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/002,800
FILING DATE: 1-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: HARTINGTON, James J.
REGISTRATION NUMBER: 38,711
REBERBENGE/DOCKET NUMBER: 4526.200-US
TELEPHONE: 212.867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: No. 59726/UO NO. JJEST STREET: 405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United States of America ZIP: 10174-6401
                                                                                                                                                                                                                                                      COUNTRY: United States of America ZIP: 10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3192 base pairs
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STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                 New York
                                                                                                                                                                                                    New York
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US-09-005-397-26
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Db 1545 GCCTCGCTGCCGTACGACCTGGGTGTGTTCCCCATCAGCGACTACTACT 1599
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VECTORS CONTAINING SAME AND METHOD FOR
THE SELECTION OF TRANSFORMANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 31.9%; Score 23; DB 2; Length 3192; Best Local Similarity 63.6%; Pred. No. 5.2; Matches 35; Conservative 0; Mismatches 20; Indels
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GENERAL INFORMATION:
APPLICANT: RHEE, Sang-Ki
APPLICANT: CHOI, Eni-Sung
APPLICANT: KIM, Chul-Ho
APPLICANT: KANG, Hyun-Ah
APPLICANT: KANG, Hyun-Ah
APPLICANT: KIM, Hwa-Young
APPLICANT: KIM, Hwa-Young
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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STREET: Keukdong Villa Ka-101, Kwangjang-dong,
STREET: Kwangjin-gu
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STREET: Dasol Apt. 102-507, #395-3, Kung-dong,
                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/706,037
FILING DATE: 30-Aug-1996
APPLICATION NUMBER: US 60/002,800
FILING DATE: 1-SER-1996
APTORNEY/AGBNT INFORMATION:
NAME: HAITINGTON, James J.
REGISTERNICATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 38,711

                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,397
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143-210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CUENGTH: 3192 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-08-903-800A-5/C
                                                                                                                                                                                                                                                                      FILING DATE:
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COCATION:
US-09-005-397-26
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                            STREET:
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                                E: KIM, Chul-Ho
Shindonga Apt. 2-1101, Yongjeon-dong, Dong-gu
                                                                                                                                                                                                                                                                                        ADDRESSEE: KANG, Hyun-Ah
STREET: Kyungseong Keunmaul Apt. 125-1501, Kalma-dong,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dehydrogenase gene of Hansenula polymorpha DL-1(ATCC 26012)
                                                                                                                                                               ADDRESSEE: SOHN, Jung-Hoon
STREET: Nuri Apt. 103-506, Wolpyung-dong, Seo-gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diskette, 3.5inch, 1.44MB storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: glyceraldehyde-3-phosphate OTHER INFORMATION: dehydrogenase gene of Hanse OTHER INFORMATION: polymorpha DL-1(ATCC 26012)
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: KIM, Hwa-Young
STREET: #3-462, Bukahyun-3-dong, Seodaemun-gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/903,800A
FILING DATE: 31-JUL-1997
CTARSTETCATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 31-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 87-3173
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 1, Application US/09036987A; Patent No. 6143526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                       RY: Republic of Korea 300-200
                                                                                                                                                                                                                                    KY: Republic of Korea
302-280
Republic of Korea
                                                                                                                                                                                                                                                                                                                                                                                               Republic of Korea
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120-190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC/AT OPERATING SYSTEM: M
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                                        ADDRESSEE:
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COUNTRY:
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                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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Db 14307 TTGAGGTCGGGACGTCCGCAGCCGCGCGACCACTCGGGAGAGGCCTGGAAGCC 14365
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Best Local Similarity 61.0%; Pred. No. 30;
Matches 36; Conservative 0; Mismatches 23; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 ttcaggacgatgcttcggtgccttaagacacctacctttgtgtctatgacatgtgagcc 62
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Patent No. 6274350

GENERAL INFORMATION:
APPLICANT: Baltz, Richard H

APPLICANT: Broughton, Mary C

APPLICANT: Crawford, Kathryn P

APPLICANT: Treadway, Patti J

TITLE OF INVENTION: 011ve

TITLE OF INVENTION: 0305ynthetic Genes For Spinosyn Insecticide

FILE REFERENCE: 50489 DIV1

CURRENT APPLICANT: NOWAER: US/09/370,700
                                                                                                                                           APPLICANT: Treadway, Patti J.
APPLICANT: Turner, Jan R.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Production
                                                                                                                                                                                                                                                                                                                                                       H: Dow AgroSciences LLC Patent Department 9330 Zionsville Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/036,987A
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EARLIER APPLICATION NUMBER: US 09/36987
EARLIER FILING DATE: 1998-03-09
NUMBER OF SEQ ID NOS: 39
APPLICANT: Baltz, Richard H.
APPLICANT: Broughton, Mary C.
APPLICANT: Crawford, Kathryn P.
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Merlo, Donald J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
REGISTRATION NUMBER: 28,479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)337-4816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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nucleic acid
DEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                          Indianapolis
                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \mathbf{u}\mathbf{s}\mathbf{a}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 80
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LENGTH: 1968
                                                                       1968
                                                                       LENGTH
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                                                                                                                                                                                  DB 4; Length 80161;
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UG-09-222-191-30/C

Sequence 30, Application US/09232191

Patent No. 6284487

GENERAL INFORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: Fatty Acid Transport Proteins
FILE REFERENCE: WHI97-21p3ME
CURRENT APPLICATION NUMBER: US/09/232,191
CURRENT FILING DATE: 1999-01-14
EARLIER FILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-01-15
SEALIER FILING DATE: 1998-01-15
SEALIER FILING DATE: 1998-12-04

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FASTSEQ for Windows Version 3.0

LENDER: NUMBER: CALLIER FILING DATE: 1998-12-04

SEQ ID NO 30

LENDER: LIGHT FASTSEQ FOR WINDOWS VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Stahl, Andreas
APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
ITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WHI97-21p3MB
CURRENT APPLICATION NUMBER: US/09/232, 200A
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/071, 374
EARLIER APPLICATION NUMBER: 60/093, 491
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20
                                                                                                                                                                                Query Match 30.8%; Score 22.2; D Best Local Similarity 61.0%; Pred. No. 30; Matches 36; Conservative 0; Mismatches
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Sequence 80, Application US/09232200A;
Patent No. 6288213
                                                                     TYPE: DNA
CRGANISM: Saccharopolyspora spinosa
US-09-370-700-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-09-232-191-30
    SOFTWARE: Patentin Ver. 2.
                       SEQ ID NO 1
LENGTH: 80161
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                                                                                                                                   Query Match 30.6%; Score 22; DB 4; Length 1968; Best Local Similarity 67.4%; Pred. No. 11; Matches 31; Conservative 0; Mismatches 15; Indels
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Sequence 80, Application US/09232201A
Fatent No. 6348321
GENERAL INFORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: LAISEN, David J.
APPLICANT: LAISEN, David J.
APPLICANT: Calcish, Harvey F.
APPLICANT: Gimeno, Ruth E.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REPERENCE: WHH97-21p3MC
CURRENT APPLICATION NUMBER: US/09/232,201A
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER APPLICATION NUMBER: 60/093,491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Stahl, Andreas
APPLICANT: Hissch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglla, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WH197-21p3MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT PARLICATION NUMBER: US/09/232,197A
CURRENT FILING DATE: 1999-01.14
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER FILING DATE: 1998-01.15
EARLIER FILING DATE: 1998-01.15
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 80, Application US/09232197A Patent No. 6300096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-09-232-197-80
TYPE: DNA; ORGANISM: Caenorhabditis elegans
US-09-232-200-80
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us-09-899-718a-4.rni

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Gaps
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Pred. No. 11;
                                                                                                                                                                                                                                                                                                                  0; Mismatches 15; Indels
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APPLICANT: Randay, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 587
TITLE OF INVENTION: Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and CREW LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) NAME/KEY: misc_feature

) LOCATION: 1..246240

) OTHER INFORMATION: /note= "HLA-H.CONTIG"

US-08-724-394A-20
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
BARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FASTSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/08724394A Patent No. 5872237 GENERAL INFORMATION:
                                                                                                                                                           TYPE: DNA
CRGANISM: Caenorhabditis elegans
US-09-232-201-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feder, John N.
Kronmal, Gregory S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: not relevant TOPOLOGY: not relevant
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67.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08 FILING DATE: 01-OCT-1996 CLASSIFICATION: 536
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Best Local Similarity 67.4%
Matches 31; Conservative
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                                                                                                                 SEQ ID NO 80
LENGIH: 1968
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                                                                                              9 gacgatgcttcggtgccttaagacacctacctttgtgtctatgacatgtgagcccaacag 68
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Score 22; DB 2; Length 246240;
Pred. No. 50;
0; Mismatches 25; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1 TITLE OF INVENTION: Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 1.246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      017957-000100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                         ; Sequence 21, Application US/08724394A
; Patent No. 5872237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFRENCE/DOCKET NUMBER: 0179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Feder, John N. APPLICANT: Kronmal, Gregory S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-576-0300 INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   not relevant
         30.6%;
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Best Local Similarity 59.79
Matches 37; Conservative
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                                                     Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid STRANDEDNESS: not r
                             Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 01 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: no
MOLECULE TYPE:
                                                                                                                                                                                                                                 Db 183667 GG 183668
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         Query Match
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RESULT 15

Sequence 22, Application US/08724394A

Sequence 22, Application US/08724394A

Sequence 22, Application US/08724394A

Sequence 22, Application US/08724394A

Sequence 23, Application US/08724394A

SPRICIANT ROUGHL INFORMATION US/08724394A

SPRICIANT ROUGHL SEQUENCES: ADMINISTRY US/087241

SEQUENCE SEQUENCES: ADMINISTRY US/087241

SEQUENCE MADERIAL TOWNSEND And CREW LIP

STRIED OF INVENTION US/087231

SEQUENCE SEQUENCES: ADMINISTRY US/087241

SEQUENCE SEQUENCES: ADMINISTRY US/087241

SEQUENCE REPRESENCE OFFICE OFFI
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July 31, 2002, 12:11:57; Search time 5855.71 Seconds (without alignments) 165.954 Million cell updates/sec US-09-899-718A-4 72 1 cctttcaggacgatgcttcg.....catgtgagcccaacagtggc 72 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. 13736207 seqs, 6748477542 residues OM nucleic - nucleic search, using sw model IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Title: Perfect score: Scoring table: Searched: Sequence: Run on:

27472414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

em_esthum:*
em_esthum:*
em_estnu:*
em_estov:*
em_estor:*
em_estp:*
em_estp:*
gb_est:*
gb_est2:*
gb_htc:*
gb_gss:*
em_gss_hum:*
em_gss_hum:*
em_gss_hum:*
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em_gss_hum:* em_estba:* EST:* 5... 110... 111... 112... 115... Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	AQ466003 HS_5139_B	BE750138 201331 MA	BF028674 601763910	BH103249 RPCI-24-2	676499 602622960	852601 1024034F0	176205 005_F_08-	613147 T7 end of	613148 T7 end of	536358 RPCI-11-3	36780 QV1-LT003	320218 RPCI11-10	716839 HS_5473_A	24309 BB524309	BF143122 601788012	785147 HS_3159_A	210823 Sm1-60D24
	Desc	AQ.	BE	BF(BH	BG	BGI	ВН	AL	AL	AQ	AWB	AQ	AQ	BBS	BF	AQ	HH
	ΙD	AQ466003	BE750138	BF028674	BH103249	BG676499	BG852601	BH176205	CNS07J0P	CNS07J00	AQ536358	AW836780	AQ320218	AQ716839	BB524309	BF143122	AQ785147	FH210823
	DB	12	10	10	12	10	10	12		13		σ		12		10		
	Query Match Length DB	450	544	877	340	930	2069	305	305	305	447	557	622	502	273	625	510	5
dР	Query	37.8	37.5	37.5	37.2	36.7	36.7	36.1	36.1	36.1	36.1	36.1	36.1	35.8	35.6	35.6	35.3	35
	Score	27.2	27	27	26.8	26.4	26.4	26	56	26	26	26	26	25.8	25.6	25.6	25.4	25.4
	Result No.		7	m	4	Ŋ	ø	7	ω	σ	10	11	12	13	14	15	16	17
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25. 2 35.0 285 9 BI 2 25.2 35.0 4713 12 2 25.3 34.7 122 110 2 25.3 34.7 225				9	AZ230592 RPCI-23-7	BE854968 ux35h10.y	9			AI592234 mr31h02.y			AQ433466 HS_5052_B		AQ722509 HS_5228_A	7	BB322109 BB322109				BG331922 602433085	0	9	20	630	æ	954	BH211493 Sm1-54L5.
18 25.4 35.3 581 12 25.2 35.0 285 9 25.2 35.0 4713 12 25.2 35.0 4713 12 25.2 35.0 482 11 25.2 35.0 482 11 22 25 34.7 193 9 25 34.7 27 9 3 25 34.7 27 9 3 3 3 2 25 34.7 27 9 3 3 3 2 25 34.7 27 9 3 3 3 2 25 34.7 27 9 3 3 3 2 25 34.7 27 9 3 3 3 2 25 34.7 27 9 3 3 3 2 25 34.7 27 9 3 3 3 2 25 34.7 27 9 3 3 3 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3	AZ941767	BB483511	AQ297755	AQ005736	AZ230592	BE854968	BF183196	AV336150	BE140819	AI592234	AA169000	AU179961	AQ433466	BM253384	A0722509	BF725277	BB322109	BJ020917	BF664154	BG484311	BG331922	R56980	BF955906	BE524520	AZ111630	AZ951598	AZ496954	BH211493
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1188	35.3	35.0	35.0	35.0	35.0	34.7	34.7	34.7	34.7	34.7	34.7	34.7	34.7	34.7	34.7	34.7	34.7	34.7	34.7	34.7	34.7	34.4	34.4	34.4				
	ω.	'n.	ω.	ω.	ω.	N	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	4	4	4	4	4	4	4
	18	19	20	21	22	23	24	25	26	27	28	58	30	31	32	33	34	35	36	37	38	39	40	4.1	42	43	44	45
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ALIGNMENTS

AQ466003 HS_5139_B2_E07_SP6E RPCI-11 Human Male BAC Library Homo saplens genomic clone Plate=715 Col=14 Row=J, DNA sequence. AQ466003 AQ466003.1 GI:4643098 GSS. Human Homo saplens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammallar Eutherla: Primates: Catafrinin; Hominidae; Homo. (bases 1 to 450) Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood. L. 	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589 Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center Onlyersity of Washington Atl Queen Anne Avenue North, Seattle, WA 98109, USA 7el: (206) 616-3887 Fax: (206) 616-3888 Fax: (206) 616-3887 Fax: (206) 616	
RESULT 1 AQ466003/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL MEDLINE COMMENT	FEATURES source

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37.5%; Score 27; DB 10; Length 877; 62.7%; Pred. No. 38;
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                               25; Indels
    62.7%; Pred. No. 33; tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NIH_MGC_53"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:3995858"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42; Conservative
                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
      Best Local Similarity
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                                                                                                                                                        62 ccaacag 68
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                                                                                             Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and partially digested with a combination of EcoRI and paAce3.6 vector at EcoRI sites 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 544)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 25-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence evaluation of four pooled-tissue normalized bovine cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 20 and day 40
                                                                                /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                     374 TCTCAGGAAAATACTTCTATGTCTTAAGTGGCCTAGCACAGTGTTTAGCACATTTG 319
                                                                                                                                                                                                                                                                                                                                                          3 tttcaggacgatgcttcggtgccttaagacacctacctttgtgtctatgacatgtg 58
                                                                                                                                                                                                                                                                        37.8%; Score 27.2; DB 12; Length 450; 67.9%; Pred. No. 27; tive 0; Mismatches 18; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
             /clone="Plate=715 Col=14 Row=J"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201331 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
BE750138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
NO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   544 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9913"
/clone_lib="MARC 4BOV"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plate: 110 row: E column: 20 Seq primer: ATTTAGGTGACACTATAG.
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FORWARD: AGGAAACAGCTATGACCAT BACKWARD: GTTTTCCCAGTCACGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovidae; Bovinae; Bos.
                                                              /sex="male"
                                                                                                                                                                                                                                                                                              Local Similarity 67.9% tes 38; Conservative
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37.5%; Score 27; DB 10; Length 544;

Query Match

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BF028674 877 bp mRNA linear EST 10-OCT-2000 601763910F1 NIH_MGC_53 HOMO SapienS CDNA clone IMAGE:3995858 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="carcinoma, cell line"
/lab.host="DH10B (T1 phage-resistant)"
/note="Corgan: bladder: Vector: DNR-LIB (Clontech);
Site_1: Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc);
bouble-stranded cDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ARTCTAGAGGCGGAGGCGGCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCGGGGGGGCATG-GT(30)BN-3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PGR. This library was enriched for Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM847 row: d column: 03
                                                                                                          DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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ACCESSION

KEYWORDS

SOURCE

VERSION

BH103249

RESULT

REFERENCE AUTHORS JOURNAL

TITLE COMMENT

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/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 29-MAY-2001
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Chlamydomonas reinhardtii.
Eukaryota: Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.

1 (bases 1 to 2069)
Grossman, A., Darkles, J., Federspiel, N., Harris, E., Lefebvre, P.,
McDermott, J.P., Silflow, C., Stern, D. and Surzycki, R.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Unpublished (2000)
Contact: Charles Hauser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="squamous cell carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG852601
1024034F08.x1 C. reinhardtii CC-1690, normalized, Lambda Zap II
Chlamydomonas reinhardtii CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.W.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.rb column: 15
1 (bases 1 to 930)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 26.4; DB 10; Length 930;
Pred. No. 63;
0; Mismatches 21; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone="IMAGE:4747838"
/clone_lib="NCI_CGAP_Skn4"
                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 842.
Location/Qualifiers
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Location/Qualifiers
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BG852601.1 GI:14233785
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Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.7%;
65.0%;
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Best Local Similarity
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          REFERENCE
                                    AUTHORS
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O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 01-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                 Lycases + Co 340, Malek, J., Shatsman, S., Akinret, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E., Mussell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
The Institute for Genomic Research
Tel: 301 838 0200
Fax: 301 838 0200
                                                                                    BH103249 340 bp DNA linear GSS 19-JUL-2001
RPCI-24-230C14.TJ RPCI-24 Mus musculus genomic clone RPCI-24-230C14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 library availability, please contact Pieter de Jong (pdejongemail.cho.org), Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end page: http://www.iigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 230 row: C column: 14
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 340)
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Best Local Similarity 68.5%; Pred. No. 34;
Matches 37; Conservative 0; Mismatches
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/clone="RPCI-24-230C14"
/clone_lib="RPCI-24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       library was cloned in a BamH1 sites using MboI DNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                        BH103249.1 GI:14930007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
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KEYWORDS
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FEATURES

BG676499

SOURCE

RESULT

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Gaps

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/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: McDir This library, constructed by John Davies and Jeffrey McDermott, combines cDNas from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in the ambient levels of CO2 and HS medium bubbled with $$ CO2. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The CDNA was directionally cloned into lambda
                                                                                                                                                                                                                                                                                       ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806." ESS c 637 g 275 t 61 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Le Paslier,M.-C., Pierce,R.J., Merlin,F., Hirai,H., Wu,W., Williams,D.L., Johnston,D., LoVerde,P.T. and Le Paslier,D.
Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library
                                                                                                                                                                                                                                  ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites. pBluescript II SK- plasmids were excised from the lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    005_F_08-21 SmBAC1 Schistosoma mansoni genomic clone 005F08 5', DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSS 29-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2017 CGATGCTCCGNCTGCTTGAGCCATCTATATGTAAANGACATCATCGAGTAAGCGTG 1958
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Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 305)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 cgatgcttcggtgccttaagacacctacctttgtgtctatgacatgtgagcccaacagtg 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10; Length 2069;
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1 rue du Professeur A. Calmette, 59019-Lille, France
Tel: (33) (0)3 20877783
Fax: (33) (0)3 20877888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23; Indels
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/lab_host="Biomphalaria glabrata"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 26.4; DB
Pred. No. 79;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 bp
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Seq primer: M13 -21 primer
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62.9%;
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Matches 39; Conservative
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/note="Vector: pBeloBAC 11; Site_1: Hind III; Partially Hind III digested and size selected S. mansoni cercarial DNA was ligated into Hind III digested pBeloBAC 11 vector and used to Transform E. coli DHIOB. The complete library contains 23808 clones from 4 independent
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Partially Hind III digested and size-selected S. mansoni cercarial
DNA was ligated into Hind III digested pBeloBAC II vector and used
to transform E. coli DH10B. The complete library contains 23808
clones from 4 independent sizing-ligation-transformations. Average
insert size ranges from 70-127 kb and genome coverage is 7.9-fold.
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(bases 1 to 305)
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/note="end : T7"
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AQ536358
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Partially Hind III digested and size-selected S. mansoni cercarial
DNA was ligated into Hind III digested pBeloBAC II vector and used
to transform E. coli DH10B. The complete library contains 23808
clones from 4 independent sizing-ligation-transformations. Average
insert size ranges from 70-127 kb and genome coverage is 7.9-fold.
    GSS 08-OCT-2001
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CNS07J0Q 305 bp DNA linear GSS 08-OCT-2001
T7 end of clone 005DC04 of library SmBAC1 from strain Puerto-Rican
of Schistosoma mansoni, genomic survey sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Lobase I to 305)
Williams, D.L. Johnston, D., LoVerde, P.T. and Le Paslier, D. Construction and characterization of a Schistosoma mansoni Denerial artificial chromosome library
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Other_GSSs: RPCI-II-318MIO.TV
Other_GSSs: RPCI-II-318MIO.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
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/organism="Schistosoma mansoni"
/strain="Puerto-Rican"
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV1-Lr0036-150 200-070-folist=22000-02-15&t4=1) Seq primer: puc 18 forward High quality sequence start: 11 High quality sequence stop: 557. Location/Qualifiers
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OV1-LT0036-150200-070-f01 LT0036 Homo sapiens CDNA, mRNA sequence.
AW836780
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 557)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Magal,M.A., ad Sllvay,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Nagal,M.A., Goldin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                          library availability, please contact Pieter de Jong (pieter@de]ong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html. Seq primer: SP6 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shorgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCIII Human Male BAC Library" 91 c 100 g 115 t
Email: bbe@tigr.org
Clones are derived from the human BAC_library_RPCI-11. For BAC
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20202663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 cttcggtgccttaagacacctacctttgtgtctatgacatgtgagcccaa 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="Lymphocytes"
                                                                                                                                                                                                                                                                                                          1. 447
/organism="Homo sapiens"
/db_xref="GDB:7622025"
                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/clone="RPCI-11-318M10"
/clone_lib="RPCI-11"
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                                                                                                                                                                                                                                                                          Location/Qualifiers
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Fax: +55-11-2707001
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Gaps

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GSS 13-JUL-1999

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High rhroughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
701 Queen Anne Avenue North, Seattle, WA 98109, USA
701 Gueen Anne Avenue North, Seattle, WA 98109, USA
701 Fax: (206) 616-3818
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703 Fax: (206) 616-3818
704 Fax: (206) 616-3818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 502)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                         AQ716839 502 bp DNA linear GSS 13-JUL-HS_5473_Al_D10_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1049 Col=19 Row-G, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                            /clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                           16 cttcggtgccttaagacacctacctttgtgtctatgacatgtgagcccaa 65
                                                       15; Indels
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67.9%; Pred. No. 85;
tive 0; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Mahairas GG, Wallace JC, Hood L
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                          Pred. No. 77;
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/db_xref="taxon:9606"
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AQ716839.1 GI:5466155
                   70.08;
                   Best Local Similarity 70.0 Matches 35; Conservative
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                                                                                                                  /note="Organ: lationlos; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
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Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Userly, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)
Other_GSSs: RPCIII_100C1_TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AWJZUZIB
RPCIII-100CI.TV RPCI-11 Homo sapiens genomic clone RPCI-11-100C1,
DNA sequence.
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Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please context Pieter de Jong
(pieter@dejong.med.bufalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.bufalo.edu/ordering) or from
Research Genetics (infc@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 75;
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Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9712 Medical Center Dr., Rockville, MD 20850
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
/clone="RPCI-11-100C1"
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                                                             /clone_lib="LT0036"
/dev_stage="Adult"
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1. .622
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Best Local Similarity 70.0%;
Matches 35; Conservative (
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Fax: 301 838 0208
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AUTHORS
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EST 28-JUL-2000
 Gaps
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                                                 317 CCTTCTGGGATATGACTGTGTTCCCAAAGGCGCCTACTTTGGGTCTAAGACA 369
                            2 ctttcaggacgatgcttcggtgccttaagacacctacctttgtgtctatgaca 54
17; Indels
                                                                                                                                                     linear
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us-09-899-718a-4.rst

SOURCE

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is I (bases 1 to 625)
is Nil-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection

Octoract: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov

Plate: LLAM9262 row; g column: 03

High quality sequence stop: 465.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF143122 625 bp mRNA linear EST 24-OCT-2000 601788012F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4015898 5',
was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 625)
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/lab_host="DH10B"
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/db_xref="taxon:10090"
/clone="IMAGE:4015898"
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Matches 43; Conserve
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, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Hivozane, T., Horl, F., Ishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Kagawa, T., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
Matuyama, T., Miki, K., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ono, T., Owa, C., Salto, H., Sakai, C., Sato, K., Shibata, Y.,
Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Shibata, Y., Shinagawa, A., Takahashi, F., Tominaga, N., Toya
, T., Tsunoda, Y., Watahiki, A., Yokota, T., Yamamura, T., Yamanaka, I.,
Yano, R., Yasuhishi, A., Yokota, T., Yoshino
RIKEN Mouse ESTS (Konno, H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genome-res@gsc.riken.go.jp,
UKL:http://qenome.gsc.riken.go.jp,
UKL:http://qenome.gsc.riken.go.jp,
N. Okazaki,Y. Nishiyama,Y. Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y. Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoacrivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
Fax: 81-45-503-9216
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                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RIKEN full-length enriched, 15 days embryo
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           BB524309 RIKEN full-length enriched, 15 days embryo head Mus musculus cDNA clone D930019D20 3', mRNA sequence.
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/dev_stage="15 days embryo"
/lab_host="DH10B"
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/db_xref="taxon:10090"
/clone="D930019D20"
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Search completed: July 31, 2002, 12:12:01 Job time: 13474 sec

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Enterococcus faeca
Human prostate tum
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DNA encoding human
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GenCore version
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                              - nucleic search, using sw model
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υ	35	m	2.5	305107	22	ААН62689	Shrimp white spot
υ	36	23.2	2.5	11628	20	AAX20520	Polynucleotide seq
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PA	(PE	EKE) PE	CORP NY	۲.			
PI	Ven	enter JC,	Adams	M, Li	PWD	Myers EW;	
X C	WPT	2001	-656860/	775			
XX			,				
PT	New	solat	ed nucleic a	eic acid	d de	detection reagent for de	r detecting 1000 or more
P.I.	genes	from	Drosop	hila an	d fo	lating cell	and

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AAC07947;
                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                    Matches
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                                                                                         capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell.cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                  (ABB57137-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000~\mathrm{or} more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1321 cetttcgcgaatatgagcatgagcctgaggagttcaaccgccgtctccaagagctgacag 1380
                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 cetttcaggacgatgettcggtgccttaagacacctacctttgtgtgtctatgacatgtgag 60
                                                                              The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                      35.6%; Score 25.6; DB 23; Length 3085; 59.7%; Pred. No. 3.7; tive 0; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genomic polynucleotide SEQ ID NO 1861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 1861; 21pp + Sequence Listing; English.
                                      Claim 1; SEQ ID NO 1864; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                 Sequence 3085 BP; 861 A; 776 C; 752 G; 696 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li PWD, Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL16796 standard; DNA; 20261 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 59.79
Matches 43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 cccaacagtggc 72
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  interactions -
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derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expressed sequence tag; secreted protein; cDNA isolation;
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                                                                                                                                                                   specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                             The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                    35.6%; Score 25.6; DB 23; Length 20261; 59.7%; Pred. No. 6.7; Live 0; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                        Sequence 20261 BP; 5591 A; 4571 C; 4371 G; 5728 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein 5' EST, SEQ ID NO: 12022.
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                                                                                                                                                                                                            at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene therapy; chromosome mapping; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43; Conservative
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                                                                                       (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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Sequence 152 BP; 26 A; 48 C; 49 G; 29 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -
                                                                              Gaps
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Score 25; DB 21; Length 152;
Pred. No. 2.5;
0; Mismatches 15; Indels
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34.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
       Query Match
Best Local Similarity 69.43
Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC00215;
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New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus

Barash SC, Dillon PJ, Kunsch CA;

WPI; 1999-045171/04.

(HUMA-) HUMAN GENOME SCI INC.

97US-0066009. 97US-0044031. 97US-0046655.

06-MAY-1997

98WO-US08985.

04-MAY-1998; 14-NOV-1997; 16-MAY-1997;

Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.

Enterococcus faecalis

WO9850555-A2

12-NOV-1998.

Enterococcus faecalis genome contig SEQ ID NO:632.

(first entry)

19-MAR-1999

AAX13569;

AAX13569/c ID AAX13569 standard; DNA; 626

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AAX12938 to AAX13919 represent these nucleotide sequences isolated from the Enterococcus facealis genome. AAX12938 to AAX13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus facealis genome with commercial importance. The products can be used to detect the presence of Enterococcus facealis in samples. They can also be used for diagnosing Enterococcus infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus facealis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus facealis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            computer readable medium has been developed which has recorded on it
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Pred. No. 3.8;
0; Mismatches 20; Indels
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Best Local Similarity 64.9%;
Matches 37; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                    Infection
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Score 25; DB 21; Length 424; Pred. No. 3.4; 0; Mismatches 15; Indels

34.78;

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Query Match Best Local Similarity Matches 34; Conserva

caggacgatgcttcggtgccttaagacacctacctttgtgtctatgaca 54

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02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
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14-AUG-2000;
18-AUG-2000;
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14-SEP-2000;
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14-AUG-2000;
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25-SEP-2000;
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30-AUG-2000;
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22-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acids derived from human pancreatic tunor tissue which have cytostatic activity. The sequences are also useful in producing pharmaceutical compositions for treatment of pancreatic tumors. AAZ52838-Z53014 represent expressed sequence tag (EST) fragments derived from a human pancreatic tumor cDNA library and which encode the proteins represented in AAY73814-Y74252.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel polypeptides and their encoding nucleic
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                                                                                Pancreas; tumor; EST; expressed sequence taq; human; cytostatic;
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                                          Human prostate tumor cDNA library derived EST fragment #148.
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69.48;
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Best Local Similarity 69.4°
Matches 34; Conservative
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Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system
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08-NOV - 2000;
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05-DEC-2000;
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13-OCT-2000;
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The Thronicon retries of the preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune chaemalytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myccardial ischaemias; (d) wound healing; (e) neurological diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                  The invention relates to novel genes (ABA11004-ABA21534) and proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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                                 Disclosure; SEQ ID NO 10456; 1701pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding human prostate cancer antigen, Seq ID No 573.
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17-MAR-2000;
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Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the reproductive system including prostate cancer and also for testing and detection e.g. diagnosis -

Disclosure; SEQ ID No 573; 546pp; English.

The invention relates to novel isolated human prostate cancer antigen polynucleotides (I) and polypeptides (II). (I) and (II) are useful for preventing, treating or ameliorating a medical condition when administered. (I), (II) and the antibody to (II) are useful for treating, preventing and/ or prognosing disorders related to the reproductive system including prostate cancers; urinary disorders e.g. chronic emperities; and blood-related disorders e.g. thrombosis. (II) can be used for testing and detection e.g. as a chromosomal marker and in forensics. (I) and the anti-(II) antibody can be used in testing and detection in immunoassays. Assi0061-Ass40775 represent the human prostate cancer antigen coding sequences, and related PCR primers and sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format

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                                 31-JAN-2000;
04-FEB-2000;
                                                       24-FEB-2000;
02-MAR-2000;
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17-MAR-2000;
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11-JUL-2000;
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14-AUG-2000;
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The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, in the prevention and resent sequence is a genomic sequence encoding a including cancer. The present sequence is a genomic sequence encoding a
                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41683.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3098 BP; 629 A; 858 C; 936 G; 675 T; 0 other;
                                                                                                                                                                                                                                                                                                                                  Rosen CA, Barash SC, Ruben SM;
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                                                   17-NOV-2000; 2000US-0249244.
17-NOV-2000; 2000US-0249244.
17-NOV-2000; 2000US-0249245.
17-NOV-2000; 2000US-0249265.
17-NOV-2000; 2000US-0249265.
17-NOV-2000; 2000US-024929.
17-NOV-2000; 2000US-024929.
17-NOV-2000; 2000US-024929.
17-NOV-2000; 2000US-0249300.
01-DEC-2000; 2000US-0251988.
05-DEC-2000; 2000US-0251988.
05-DEC-2000; 2000US-0251988.
06-DEC-2000; 2000US-0251868.
                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
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08-DEC-2000; 2000us-0251989.
08-DEC-2000; 2000us-0251990.
                    17-NOV-2000; 2000US-0249216.
17-NOV-2000; 2000US-0249217.
                                                                                                                                                                                                                                                                      11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
                                  17-NOV-2000; 2000US-0249217.
17-NOV-2000; 2000US-0249218.
2000US-0249214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein of the invention.
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Ruben SM;
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2000US-0249215.
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2000US-0254097
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2000US-0246475
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                     02-0CT-2000;
03-0CT-2000;
04-0CT-2000;
06-0CT-2000;
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05-DEC-2000;
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05-DEC-2000;
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08-DEC-2000;
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AAK AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1)
aniho acid sequences given in AAM82170 to AAM91921. (1) have cytostatic
activity, and can be used in gene therapy and vaccine production. (1)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (1) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectlifying mutations or deletions in a patient, s genome
complement the patients own production of (1). Additionally, (1)
that affect the activity of (1) by expressing inactive proteins or to
supplement the patients own production of (1). Additionally, (1)
coplynucleotides may be used to produce the secreted (1), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (1) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-derived cells. AAK64703
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54912 to AAK6750 and AAM82169
crepresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ovarian tumour marker gene; human; overexpression; upregulation; epithelial tumour; cancer; diagnosis; prognosis; disease monitoring; identification; serous cystadenoma; borderline serous tumour; serous cystadenocarcinoma; mucinous cystadenocarcinoma; mucinous cystadenocarcinoma; mucinous cystadenoma; borderline mucinous tumour; endometriold carcinoma; undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma; serner tumour; serial analysis of gene expression; SAGE; immune response pathway; cell proliferation regulation; protein folding; membrane localised; secreted; therapeutic target; cytostatic; gene therapy; vaccine; ds.
Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                            Disclosure; SEQ ID NO 41683; 3071pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hondh CD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HLA-Cw ovarian tumour marker gene, SEQ ID NO:81.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABA83122 standard; DNA; 4316 BP
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Best Local Similarity 69.4's
Matches 34; Conservative
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P-PSDB; ABB50296.
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                                                                                                                        The invention relates to methods for diagnosing and prognosing ovarian tumours in an individual via the detection and measurement of the expression of ovarian tumour marker genes (ABA83182-ABA83122, ABA83189, ABA83182 and ABA83184) or segments thereof (ABA83123-ABA83189, ABA83189, ABA83181 and ABA83183). The methods of the invention are useful for detecting an ovarian tumour in a patient, for identifying an individual at increased risk for developing ovarian cancer, in prognostic tests for monitoring a patient in remission from ovarian cancer and in tests for monitoring disease status in a patient being treated for ovarian cancer. The methods can additionally be used to identify a particular tumour as being an ovarian tumour (i.e., an epithelial ovarian tumour selected from serious cystadenocar beautien and additionally a patient being tumour selected from serious cystadenocar beautien and additionally a patient being an ovarian tumour selected from serious cystadenocarcinoma,
                                                                                                                                                                                                                                                                                                                                                                        clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner tumour. The ovarian tumour marker genes of the invention were identified using SAGE (serial analysis of gene expression) and were found to be overexpressed in a broad variety of ovarian epithelial tumour cells relative to normal ovarian epithelial cells. The marker genes are implicated in immune response pathways, in the regulation of cell proliferation and in protein folding, and many of these are membrane-localised or secreted. In addition to their use as diagnostic and prognostic markers, the ovarian tumour marker genes or their encoded proteins may be used as therapeutic targets for the treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Nucleotide R is present at this location in the sequence shown in sequence listing of the specification" 4067.4528
             Detecting and identifying ovarian tumor, identifying increased risk for developing ovarian cancer, and determining effectiveness of ovarian cancer treatment, by measuring expression level of ovarian tumor marker
                                                                                                                                                                                                                                                                                                                                           mucinous cystadenoma, borderline mucinous tumour, mucinous cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prevention of ovarian cancer. Sequences ABA83081-ABA83122, ABA83180, ABA83180 and ABA83184 represent the ovarian tumour marker genes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; glutamate receptor metabotrophic 3; GRM3; neuroprotective;
nootropic; gene therapy; neurotransmitter; chromosome 7q21.1-q21.2;
drug screening; neurological disorder; polymorphism; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4316 BP; 1000 A; 1090 C; 1292 G; 934 T; 0 other;
                                                                                                Claim 23; Page 124-126; 140pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention.
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                                                                                                                                                                                                                                                                                                                                                                                                    Jobs "Nucleotide Y is present at this location in the sequence shown in sequence listing of the specification" 26032..50000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Nucleotide M is present at this location in the sequence shown in sequence listing of the specification"
                                                                 /note= "Nucleotide R is present at this location in the sequence shown in sequence listing of the specification"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide, a polymorphic variant of glutamate receptor, metabotrophic 3 (GRM3) gene for expressing GRM3 protein isoform to screen drugs to treat GRM3 activity-related disease
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                                                                                                                                                                                                                                                                                                                                          replace (25586, T)
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replace (4192, A)
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Matches 36; Conservative
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Thu Aug 1 08:30:01 2002

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Tanguay DA;
                                                                                                                                    (GENA-) GENAISSANCE PHARM INC.
                                                                                                                             16-JUN-2000; 2000US-212328P.
                                                                                                                      18-JUN-2001; 2001WO-US19447
      26-MAR-2002 (first entry)
                                                                                  (PS) 3"
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25586
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                                                                                                        WO200196350-A2
                                   Homo sapiens.
                                                                                       misc_feature
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AAD26437;
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polymorphic variant of glutamate receptor, metabotrophic 3 (GRM3)
isogene. GRM3 is a receptor for glutamate, the major excitory
isogene. GRM3 is a receptor for glutamate, the major excitory
neurotransmitter in the mammalian central nervous system. Human GRM3
clocated on chromosome 742:1-142:12 is expressed in human foetal and adult whole brain especially in the caudate nucleus and corpus collosum. GRM3
DNA is useful in gene therapy and also for studying the expression and function of GRM3 GRM3 polypeptide is used for screening drugs. A recombinant non-human organism is used to study expression of GRM3 GRM3 brotein, and for testing the efficacy of therapeutic agents and compunds for neurological disorders in a biological system. GRM3
compounds for neurological disorders in a biological system GRM3
chaplotypes are for treating diseases associated with GRM3 activity, e.g., neurological disorders. The present sequence is an allelic variant
compounds for the grammate containing polymorphic sites (PS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
"This degenerate base represents polymorphic site
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"This degenerate base represents polymorphic site
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/note= "This degenerate base represents polymorphic site
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/note= "This degenerate base represents polymorphic site
Human GRM3 gene fragment #1 allelic variant containing polymorphic site.
                                                                                            Human; glutamate receptor metabotrophic 3; GRM3; neuroprotective; nootropic; gene therapy; neurotransmitter; chromosome 7q21.1-q21.2; drug screening; neurological disorder; polymorphic site; PS; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide, a polymorphic variant of glutamate receptor, metabotrophic 3 (GRM3) gene for expressing GRM3 protein isoform to screen drugs to treat GRM3 activity-related disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to an isolated polynucleotide which is a
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence data for this patent did not form part of the invention. Note: The sequence data for this patent did not form part of the contacting from a the propositional information is a single exon nucleic acid probe of the invention. Once: The sequence data for this patent did not form part of the invention of form with a patent directly form with a present sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New spatially-addressable set of single exon nucleic acid probes,
useful for measuring מפחף בארחים ביות יה ביבילילים
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                                                                                                                                                                                                                                                                                                                                  Human; microarray; single exon probe; gene expression; breast;
7 aggacgatgcttcggtgccttaagacacctacctttgtgtctatgacatgtgagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for measuring gene expression in sample derived from breast, comprises number of single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 2605; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                     Human breast cell single exon nucleic acid probe #2605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanzel DK, Chen W, Rank DR;
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30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0628266.
21-SEP-2000; 2000US-0224687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US00662.
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                                                                                                                                                          ABA43910 standard; DNA; 479
                                                                                                                                                                                                                                                  (first entry)
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Gaps

Score 24.6; DB 24; Length 50000; Pred. No. 22; 0; Mismatches 19; Indels 0;

34.2%;

Query Match
Best Local Similarity 65.53
Matches 36; Conservative

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Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 2668; 639pp + sequence listing; English.
                                                                                                                                                                                                                                               Human foetal liver single exon nucleic acid probe #2668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 479 BP; 126 A; 134 C; 82 G; 137 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn SG, Hanzel DK, Chen W, Rank DR
                                                                                                                                                       ABA54363 standard; DNA; 479 BP.
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30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                  01-FEB-2002 (first entry)
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                                             62 ccaacagtg 70
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ABA54363/c
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0, Mismatches 28; Indels

Ouery Match 33.6%; Score 24.2; DB 22; Length 479; Best Local Similarity 59.4%; Pred. No. 7.4;

41; Conservative

Matches

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62 ccaacagtg 70

CCCTGAGAG 4

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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                                            July 31, 2002, 14:00:51; Search time 6034.22 Seconds (without alignments) 249.694 Million cell updates/seç
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synthetic construct
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                                                                                                 Sprunck,S., Kluth,A., Becker,D., Luetticke,S. and Loerz,H. Promoters of gene expression in plant caryopses Patent: WO 02027B5-A 4 10-JAN-2002; Aventis CropScience GmbH (DE)
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            /organism="synthetic construct"
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                              Submitted (16-JAN-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
                                                                                                                           Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzea.

1 (bases 1 to 147220)
                                                                                                                                                                                                                                              HTG; HTGS_PHASE2
                                                                                                                                                                                                                                                                                                                     AP004636 147220 bp DNA linear HTG 17-. Oryza sativa chromosome 8 clone P0685B10, *** SEQUENCING IN
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(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/.
Tel:81-298-38-7441, Fax:81-298-38-7468)
                                                                                             Direct Submission
                                                                                                           Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                            Oryza sativa
                                                                                                                                                                                                                        Oryza sativa (cultivar:Nipponbare) DNA, clone:P0685B10.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* This sequence will be replaced
Homo sapiens chromosome 5 clone CTD-2019N2, complete sequence {\tt AC008775}
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DOE Joint Genome Institute and Stanford Human Genome Center.
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On Aug 15, 2001 this sequence version replaced gi:13162501
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DOE Joint Concerts 15979)
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1 (bases 1 to 196599)

Birren, B., Linton, L., Nusbaum, C. and Lander, E. Birren, B., Chromosome 2, clone RP11-528K12
                                                                                                                                                                                                                                                                196599 bp
Homo sapiens chromosome 2 clone
SEQUENCE, 22 unordered pieces.
ACO37494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (23-AUG-2001) DOE Joint Genome Institute, 2800 M. Drive, Walnut Creek, CA 94598, USA On Aug 23, 2001 this sequence version replaced gi:11079405 Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STS Content:
SHGC-103233 G57536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.5% of Sequence;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (26-NOV-2000) DOE Joint Genome Institute, Drive, Walnut Creek, CA 94598, USA 5 (bases 1 to 195979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute.
                                                                      Unpublished
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHGC-78846 G48644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Estimated Total Number of Errors is 0.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Finishing Completed at Stanford Human Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                            HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                           AC037494.3 GI:10047908
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                                                      (bases 1 to 196599)
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/db_xref="taxon:9606"
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Stange-Thomann.N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
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Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., Lancoque, K., Lamazares, R., Landers, T., Lehoczky, J.,
Tarkey, T., Lancoque, K., Lamazares, R., Landers, T., Lehozzky, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Sep 10, 2000 this sequence version replaced gi:8017214.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Young, G., Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as
runs of N. but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 185345 bases at least Q40
Consensus quality: 189073 bases at least Q30
Consensus quality: 19263 bases at least Q20
Insert size: 208000; agarose-fp
Insert size: 194499; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality coverage: 4.3 in Q20 bases; agarose-fp Quality coverage: 4.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: M13; M77815; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center clone name: 528_K_12
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  31307 31406:
                                                    25372 25471:
                                                                                                      22238 22337:
                                                                                                                            18393 18492: gap of 100 bp
18493 22237: contig of 3745 bp in length
                                                                                                                                                                                                                14841 14940:
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                                                                                                                                                                                                                                                                                                                                                                   5531 5630: gap of 100 bp
5631 7168: contig of 1538 bp in length
7169 7268: gap of 100 bp
7269 8574: contig of 1306 bp in length
8575 8674: gap of 100 bp
                                                                                                                                                                                                                                                                                                                      9936 10035:
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                      171: gap of 100 bp
31306: contig of 5835 bp in length
                                                                          337: gap of 100 bp
25371: contig of 3034 bp in length
                                                                                                                                                                   18392: contig of 3452 bp in length
                                                                                                                                                                                                                                                               )35: gap of 100 bp
11861: contig of 1826 bp in length
561: gap of 100 bp
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145315 161113: contig of 15799 bp in length
161114 161213: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108128 108227: gap of 100 bp
108228 125265: contig of 17038 bp in length
125266 125365: gap of 100 bp
125366 145214: contig of 19849 bp in length
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82276 108127: contig of 25852 bp in length
108128 108227: gap of 100 bp
108228 125265: contig of 17038 bp in length
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50747 58275: contig of 7529 bp in length
58276 58375: gap of 100 bp
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36290 36389; gap of 100 bp
36390 42370; contig of 5981 bp in length
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42471 50646: contig of 8176 bp in length
                                                                                                                                                                                                                                      42471.
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8675. .9935
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145315. .161113
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546: gap of 100 bp
82175: contig of 70 bp
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                                                              Dugan, Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagq, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, C., Harris, C., Harris, M., Haylak, P., Hawes, A., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jonkson, E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M., Ledder, R., Morgan, M., Morris, S., Moser, M., Nekerson, J., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Peters, L., Pickens, R., Primus, E., Pu, Li., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Rison, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Sisson, I., Susani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Finnas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R.,
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Rattus norvegicus
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Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., ViWall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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norvegicus clone CH230-127L5, *** SEQUENCING IN PROGRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (23-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:16327658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
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NOTE: This is a 'working draft' sequence. It currently consists of 63 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as soon as it is available and the accession number will be preserved.
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Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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RESULT 10
AC092662
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ORGANISM
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Best Local Similarity
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8720 bp DNA linear PRI 18-SEP-Bomo sapiens chromosome 2 clone RP11-569P21, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (18-SEP-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                             Drafting center: WIBR
                                                                                                                                                                                                                                                                                                                                                                            Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                           Contact: submissions@watson.wustl.
                                                                                                                                                                                                                                                                                                                                                                                                                        Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                           Center code: WUGSC
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On Sep 18, 2001 this sequence version replaced gi:7331466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 8720)
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AC096578.1 GI:15638880
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                                                                                                                                                                                                                                            /chromosome="2"
/clone="RP11-569P21"
                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                         37.8%;
67.9%;
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contig
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gap of unknown length
contig of 1182 bp in length
gap of unknown length
                                                                                                                                                                                                                           1362 g
                                                                                                                              0; Mismatches
                                                                                                                                         Score 27.2;
Pred. No. 11;
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Pred. No. 8.
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                                                                                                                                                           Length 8720;
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                                                                                                                                                                                                                                                                          276 TCTCAGGAAAATACTTCTATGTCTTAAGTGGCCTAGCACAGTGTTTAGCACATTTG 331
                                                                                                                                                                                                                                                                                               3 tttcaggacgatgcttcggtgccttaagacacctacctttgtgtgtctatgacatgtg 58
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                        Norway rat.
                                                                                                          AC095124.2 GI:17942027
                                                                                                                                                               Rattus norvegicus clone CH230-8N7,
                                                                                                                                                                                     AC095124
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Submitted (23-OCT-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Oct 20, 2001 this sequence version replaced gi:14916246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (19-JUL-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                           46 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: submissions@watson.wustl.edu
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Submitted (20-OCT-2001) Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drafting center: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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AC092662.2 GI:16303564
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                                                                                          HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="RP11-510H11"
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67.9%;
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Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                                                        DB 9; Length 198230;
                                                                                                                                           DNA linear ... -. *** SEQUENCING IN PROGRESS ***,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C.,
Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J.,
Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
Lewis, L. Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
Loulseged, H., Lozado, R. J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
Martinez, E., Massey, E., Mawhiney, E., McLeod, M. P., Meador, M.,
Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K.,
Morgan, M., Nguyen, N., Nickerson, E., Nwokenkwo, S.,
Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B.,
Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L.,
Oulles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M.,
Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N.,
Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H.,
Sisson, I., Sutton, A., Syatek, A., Tabor, P., Tamerisa, K.,
Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N.,
Wall, R., Wang, S., Warde, Moore, S., Warren, R., Washington, C.,
Walliams, G., Williamson, R., Washington, C.,
Weinstock, G. and Gibbs, R.
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E 1 (bases 1 to 102053)

E Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Burcht, P., Burkett, C., Burcell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy, Carroll, L., Decrick, D., Davy, Carroll, L., Decrick, D., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Daraper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J. H., Guevara, W., Gunaratne, P., Hale, S., Harniandez, C., Harris, K., Hart, M., Haylak, P., Hawes, A., Hernandez, T., Hernandez, O., Hodgson, A., Hodnes, M., Holloway, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:15625678.
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Consensus quality: 80643 bases at least Q40 Consensus quality: 86605 bases at least Q30 Consensus quality: 91484 bases at least Q20 Estimated insert size: 80824; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 1.5x in Q20 bases; sum-of-contigs estimation
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.helpebcm.tmc.edu/
                                                                                                                                                                                                                                                                                                     Center project name:
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 46 contigs. The true order of the pieces is not known and their order in this sequence record is

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* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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AP003236
                                                                                                                                    Published Only in Database (2001) In press 2 (bases 1 to 167399) Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                     Oryza sativa
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                                                                                                                                                                                                                                                                                                                               AP003236.3 GI:15528647
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       on Sep 7, 2001 this sequence version replaced gi:14149142. Genes were predicted from the integrated results of the following: GENSCANI.0, BLASTN2.0, BLASTN2.0 as well as SplicePredictor
                                                  Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/.Tel:81-298-38-7441, Fax:81-298-38-7468)
                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                         Submitted (19-FEB-2001) Takuji Sasaki, National Institute of
                                                                                                                                                                                                 Oryza sativa nipponbare(GA3) genomic DNA,
                                                                                                                                                                                                               Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                                                          Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                            Direct Submission
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                                                                                                                                                                                      one:P0043B10
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102053: contig of 1024
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62.7%;
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 Mismatches

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of 1722
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of 1570
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of 1173
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A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.

The orientation of the sequence is from SP6 to T7 of the PAC clone. This sequence of P0043B10 clone has an overlap with P0560B06 clone (DDBJ: AP0032B1) at the position 1 to 117,634 of 5' end and an overlap with P0493G01 clone (DDBJ: AP002914) at the position 118,594 to 167,399 of 3' end. The sequence of this clone starts at the position 44,087 of P0560B06 and ends at the position 48,806 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (October 1998 version). The genomic sequence was searched against NCBI NonRedundant Protein database, nr (ftp://ncbi.nlm.nih, gov/blast/db) and the cDNA sequence database at RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP2.0. ESTs represent the identified of the recommendation of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP2.0. ESTs represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             p0493G01. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="P0043B10.1"
complement(10234..11904)
/gene="P0043B10.2"
                                                                                                                                                                                                                                                                     NKIGSGTYSNVYRARDTVSGRIVALKKVRFDNLEÞESVKFMAREILILRKLDHPNVIK
LEGLVVSRMSGSLYLVFEYMEBDLAGLAASÞDVKFTLPQIKCYVQOLLSGLEHCHNNN
VLHRDIKGSNLLLDNNGILKIADFGLATFFDPRKRFMTSRVVTLMYRPPELLLGATO
YGVGVDLMSAGCILAELLHGKDIMPEGREVEQUHKIFKLGGSÞSEEYMKKSKLHHATI
FKPQQPYKRGIREAFKDFPPSSLPLVETLLAIDÞÆRGTATSALQSEFFATEYYACDÞ
FKPQQPYKRGIREAFKDFPPSSLPLVETLLAIDÞÆRGTATSALQSEFFATEYYACDÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="putative CRK1 protein"
/protein_id="BAB64715.1"
/protein_id="BAB64715.1"
/db_xref="GI:15528648"
/tans1ation="MGCVFGRPSSSPPAAARKGRRKKRSSPMPAPSTDSPAADQSPG
/trans1ation="MGCVPAPAAAEQIAAGMPPWLVAVAGEALRGWTPRRADTFEKL
RGRPRRRLGRKPGPRQGCVPAPAAAEQIAAGMPPWLVAVAGEALRGWTPRRADTFEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(13564...13875,14001...14285,14372...14689,17077...17304,
18162...18262,19937...20054,20838...21152)
/gene="p0043B10.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pseudogene, similar to putative polyprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(862.
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/gene="P0043B10.1"
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/cultivar="Nipponbare"
/db_xref="taxon:4530"
/chromosome="1"
                                                                                                                                                        ANLDORRRMITHANAKSKSEKFPPPHODGAMGNPLGSSRHMEPMYEHODASFSTVVPI
OKGSSOTWSGPLVDPAALGOSRRKKOTALDAKAAAYSKOLOKOKGGTRAR"
                                                                                                                                                                                                                                                SSLPTYPPSKEMDAKMRDEEARRLRAAAKAKGEGVKRTRTRDRSQRAGPAPEANAELQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probably inactive due to stop codon(s) in CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pseudogene, similar to putative polyprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probably inactive due to stop codon(s) in CDS
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                                 join(24290. .24311,24605.
/gene="P0043B10.4"
join(24290. .24311,24605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="probably inactive due to no initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="probably inactive due to no termination codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="contains ESTs C74868(E60528),AU031247(E61207)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="P0043B10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /pseudo
/gene="P0043B10.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ′gene≃"P0043B10.3"
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2. .18262,19937. .20054,20838. .21152)
                                          .24781,25674. .25883,27639.
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AAAAGBAAGGEEEVÜBEELI AVTTGAGADEEEESGAAAAAPGBGDEESGSTEDDEA
VVGEDDDADEAEGGAVVGKREKARKKOK IQEILDTQNAAVDAMNINKGKR
LKYLLQQTEIF AHFAKGNQSKEKKPRGRGRHASKMTEEEEDEEYLKEEEDALAGSGGT
RLSQDFCI KCKMRDYQLAGLMWI KEIQRFCPILRAVKILADEMGLGKTIQTISILGYLHEEF
RGITGPHMVVAPKSTLGNWI KEIQRFCPILRAVKFLGNBEERNHI RENLLQPGKFDVC
VTSFEMAI KEKTTLKRESWRY I I I DEAHRI KNENSLLSKIMR I YMNY RILLITGTFLQ
NULHELWSLLWFLLFDIFTSSAETFDEWFGI SGENDQDEVVQQLHKVLRFPLLRERKSD
VEKGLPPKKETI LKVCMSQMQKQYYRALLQKDLEV I NAGGEKKLLNI AMQLRKCON
PYLFQGAEFGP PYTTGEHLVENAGKMYLLDKLLPKLKDDSRVLI FSQMTRLLDILED
YLMYRGYQYCR I DGNTGGEDRDAS I EARK WEGSEK VFLLSTRAGGLGI NLATADVVV
LYDSDWNPQADLQAQDRAHRIGQKKEVQVFRFCTEYT I EKVI I EARX KKLALDALVI Q
QGRLAEQKTVNKDDLLQMVRFGAEMVF SSKDSTI TDED I DRI I AKGEETT AELDAKMK
KFTEDA I KFKMDDT AELY DFDDDKFGSLLNIS I Y I LDF LKEENKLDFKKLVSDNWI ESP
RRERRRNYSSEEYFKQALRQGAPAK PREPRI PRAMPHLIDF OFFNNGARLNELY EKKVFR
LMQANQKDT LDGEDDDQLEPLTAEEQEEKEQLLEEGFATWTRRDFNTF I RACEKYGR
NDIRSJAAENEGKTEEEVQR YAKLYFKERYKELGDYD RI I LKNI I ERGEAR I SRKDEIMRA
TOTAL DE ANGERGKTEEEVQR YAKLYFKERYKELGDYD RI I LKNI I ERGEAR I SRKDEIMRA
TOTAL DE ANGERGKTEEEVQR YAKLYFKERYKELGDYD RI I LKNI I ERGEAR I SRKDEIMRA
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//gene="p0043B10.5"
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31293. 31471,31621. 31786,31880. 31938,32031. 32073,
32251. 33320,32424. 32513,32587. 32708,32743. 32774,
32842. 33030,33114. 33207,33291. 33378,33464. 33684,
33890. 33963,34047. 34329,34421. 34555,44687. 34908,
34995. 335174,35271. 35368,35488. 35600,36122. 36225,
36366. 36488,36823. 37158))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="p0043B10.6"
complement(join(37610. .37736,37900. .38138))
/gene="p0043B10.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLSIVDHAGFHKFCDVLQPLFKLMSRNTIRKDILEVLTWVKEKRPSVTNTWMIKEVDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="mrprkrgtpvTtpnTnSkDTnvIEIDDDVAVGnKrKLKYAIWQE
FGQVKVGNVWKAKCSWCQKLLSGNSGGCPHHSVMLETHVFDQNLARKKLALMICLHEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probably inactive due to no initiation codon in CDS"
                                                                                                                                                                                                                                              /note="hypothetical protein
similar to Arabidopsis thaliana chromosome 5, MXM12.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="GI:15528651"
/tianslation="MTSNVSIDDGPTATNRGLGPFVGRTRMQNIVEPNRLRPVRTDPN
PKSAGGMPQTHPRLVGGMAPPTSLLLNTLRTRGLRLRSAMKALPLLPLVVFLFETDI
SFAAVLEDFVAKPENFWEN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(37610. .37736,37900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGKKLDRYKNPWLELKIQYGQNKGKFYNEECDRFMLCMVHKLGYGNWDELKAAFRMSP
LFRFDWFVKSRTTQELARRCDTLIRLVEKENQEYDEQERQARKDKRMAKNMTPTKRSA
LRVSEGETTPSNSFKBRRQSLMDDYVGSGRRKBG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative DNA-dependent ATPase"
/protein_id="BAB64717.1"
/db_xref="GI:15528650"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="P0043B10.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="hypothetical protein
                                   /translation="MAGLAAARELRREGLDVTVLEQSADVGGQWLYDAATDGRDPLGM
AGVHSSIYSSLRLNSPREVCGFSDFPFRPTNGGGGDARRYPVHGELLRYIREFCDVFG
                                                                                                                                                                                                                                                                                                                              join(39502. .40202,40249. .40864)
/gene="P0043B10.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="contains EST C74714(E50551)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(39502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MAKPVKYDEEEEEVSSSGEEEEEQSDGAGSGSGEEEDEEEEEAP/
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LMDAVRLDTTVVRVAMAPPRRDGSLRWTVRSKHNGDAETEEVFDAVVVATGQYSQPRL
                                                                                                                  /protein_id="BAB64719.1"
/db_xref="GI:15528652"
                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="BAB64718.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                "P0043B10.7"
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RESULT :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 tcaggacgatgcttcggtgccttaagacacctacctttgtgtctatgacatgtgagccc 63
                                                                                                                                                                                                                                                                  On Mar 28, 2001 this sequence version replaced gi:11191987. Genes were predicted from the integrated results of the following: GENSCANI.0, BLASTN2.0, BLASTX2.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against when the contract of the contract
                                      RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP2.0. ESTs represent the identified cDNA sequences using BLASTN 2.0 with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (15-NOV-2000) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (cultivar:Nipponbare) DNA, clone:P0493G01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AP002914.2 GI:13486690
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corresponding DDBJ accession no. and RGP clone ID.
                                                                                                                                                                                                                                         NCBI NonRedundant Protein database, nr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Only in DataBase (2000) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spermatophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 167587)
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                                                                                                                                                                               /ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(47257. .47309,47457. .47625,47935. .48079,48190. .48309,
48945. .49010,50162. .50349)
/gene="p0043B10.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (43356.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="P0043B10.8"

complement/10075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="BAB64721.1"
/db_xref="GI:15528654"
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/gene="P0043B10.9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APSLSFVGIPVKVILPRFAEVQARWVAQVLSGRRTLPSPGEMLRAVEEYNRAKEAAGL
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66.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 20; Indels
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167587 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLN 29-MAR-2001
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FEATURES
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                                                                                                                                                                                                                                                                                                             gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.
The orientation of the sequence is from SP6 to T7 of the PAC clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MAPMKVYGWVVSPWMARVLVALEEAGAEYEVVPMSRSGGDHRRP
EHLARNPFGEIPVLEDGDLTLYQSRAIARYIFRKYKPEFLGLGEGGSLEESAMVDVWL
DVEAHQHEAAVRPILMHCIINKFEGRDRDQGVVDESVRKLEKVLGVYEARLSGSRYLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(5920. .6398,6616. .6664,6958. .7107))
probably inactive due to no initiation probably inactive due to stop codon(s)
                                                                                                             49182.
                                                                                                                                                                                                                                                 complement(34417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(28447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(5920. .6398,6616. .6664,6958. .7107))
                                                                                                                                                                                                                                                    /gene="P0493G01.5"
complemen+/^...
                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="p0493G01.4"
/note="prober"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(28447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (20654.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDRISLADLSHFSNMRYFMATEYAGVVDAYPHVKAWWEALLARPTVQKVMAGMPPDFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative glutathione S-transferase"
/protein_id="BAB39927.1"
/db_xref="GI:13486691"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D28287(R0596)
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                                                                                                                                                                                                /gene="P0493G01.5"
/note="noch-"
                                                                                                                                                                                                                                                                                                                                                              pseudogene, 12-oxophytodienoate reductase OPR2'
                                                                                                                                                                                                                                                                                                                                                                                                                  probably inactive due to no initiation/termination codons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(20654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /chromosome=":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:4530"
                                                      note="probably inactive due to frameshift(s) in
                                                                                      /gene="P0493G01.6"
                                                                                                                                                                pseudogene, mutator-like transposase"
                                                                                                                                                                                                                                                                                                                                    /pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                            note="probably inactive due to frameshift(s) in CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="P0493G01.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="P0493G01.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pseudogene, 12-oxophytodienoate reductase OPR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="probably inactive due to frameshift(s) in CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="P0493G01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="BAB39928.1"
/db_xref="GI:13486692"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="contains EST D15357(C0514)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="P0493G01.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'gene="P0493G01.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="contains ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="P0493G01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="P0493G01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Oryza sativa"
                                                                                                                                                                                             'note="probably inactive due to frameshift(s) in CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MASPYGYYGYCQERHSAVFDLAGCGFEEEGYPVVDYESALQTAK"
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                            in CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                         /translation="WTVVRRGNVRTTPQPSSGSDLERPCQNLGSTAITSVRTNCHARN FYPKRGTLTCSLTRATPNPHIQHHCRTLPLWNDCKDL" complement(join(73563.73631,73893.74134,74182.74314))/gene="P0493G01.13"
                                                                                                                                                                                                                                                                                                                                                                                                         /gene="P0493G01.10"
join(67720. .67754,68296. .68374,68468. .68516,69708.
/gene="P0493G01.11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="BAB39931.1"
/db_xref="GI:13466695"
/tzanslation="MHYDGODTWHTMEVICAYGMRSRIWKESKFGMIGYVKFVSCTR
GEPKVFWTLSMSLVRGFRLPISCINRGRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="P0493G01.9"
57009. .57230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GFPKVFWTLSMSLVRALGCLPHV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54115. .54318
/gene="P0493G01.8"
54115. .54318
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EVEAHQYYPALSPIVFECIIFPIMRGVPTNQQVVHESLEKLKKVLETYEARLSGSRYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(52409. .52866,53006. .53054,53155.
/gene="P0493G01.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(52409.
/gene="P0493G01.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /pseudo
49182. .
complement(join(73563. .73631,73893. .74134,74182. .74314))
/gene="P0493G01.13"
/note="hypothetical protein"
                                                                                                                                                                                                                                           Join(67720. .67754,68296. .68374,68468.

Jegene-*p0493G01.11*

Join(72007. .72166,72353. .72432,72937.

Jegene-*p0493G01.12*

Join(72007. .72166,72353. .72432,72937.
                                                                                                                                                                                                                                                                                                                                                                   /note="probably inactive due to stop codon(s) in CDS
pseudogene, glutathione transferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probably inactive due to stop codon(s) in CDS
pseudogene, similar to non-LTR retroelement reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="P0493G01.10"
/note="probably inactive due to frameshift(s) in CDS
probably inactive due to no initiation/termination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="contains ESTs AU065507(C0785),AU081546(C0785)unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGDFLSFADLNHFPFTFYFMATPCASLFDAYPHVKAWWEGLMSRPSIKKISANMPTKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative glutathione transferase"
/protein_id="BAB39929.1"
/db_xref="GI:13486693"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pseudogene,
P0031E09.5"
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join(67720.
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/db_xref="GI:13486694"
/trans1ation="MHVVDGDSIWHTMEVLCAYGMQSRIWKDTKFDMIGYVKFVSCTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="P0493G01.6"
                                                                                                                                           /protein_id="BAB39932.1"
/db_xref="GI:13486696"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="P0493G01.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="P0493G01.8"
                                                                                                                                                                                     /codon_start=
                                                                                                                                                                                                      /note="hypothetical protein"
                                                                                                                                                                                                                            /gene="P0493G01.12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="contains ESTs AU065507(C0785), AU081546(C0785)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MSPVKVFGRAISTNVSRVLVCLEEVGADYELVTVDFLAGEQNSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .52866,53006. .53054,53155.
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                                                                                                                                                                                                                                                                                                                              68516,69708.
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Matches
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les 39; Conserv
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                                                                                                                                                                                   Direct Submission
Submitted (15-NOV-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
5 (bases 1 to 72045)
                                                                                                                                                            5 (bases 1 to 72045)
Waterston, R.H.
                                                                                                                                                                                                                                                                                      MO 63108, USA
4 (bases 1 to 72045)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (29-JUN-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                         3 (bases 1 to 72045)
Waterston, R.H.
  Direct Submission Submitted (10-JAN-2002) Department of Genetics, Washington
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                                                                                                  Submitted (03-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sun,H., Kozlowicz,A., Elliott,G. and Doebber,A.
The sequence of Homo sapiens BAC clone RP11-811J9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Toward a complete human genome sequence genome Res. 8 (11), 1097-1108 (1998)
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Sulston, J.E. and Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                          Waterston, R.
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/db_xref="GI:13486697"
/translation="MYGSATTSAPAATRAARTAQARRRTTARGREORTPTDRGRRGELT
GRSGGGDRVDGGDGAPAVFGGGEGADEDGDDLAIPMVATATDDGGCNGGAARLNRRQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(80225.
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/gene="p0495601.14"
/note="contains ESTS C72648(E2001),C71850(E0464)
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="P0493G01.15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(77841. .80288)
/note="3' LTR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="BAB39934.1"
/db_xref="GI:13486698"
/translation="MVGCEHMVLRVVLMTIKDRFTSFGCETLTVPTTSQRGQRLYLLY
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complement/7600
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                                                                                   USA
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                                                              1 to 72045)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The clone sequenced to the left is RPI1-563K23; the clone sequenced to the right is RPI1-998A10, 2000 bp overlap. Actual start of this clone is at base position 1 of RPI1-811J9; actual end is at base position 140619 of RPI1-298A10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from processing the control of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Nov 15, 2001 this sequence version replaced gi:15625026.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence derived from pcr, base position 6122 to 6452 and 7046 to 7087.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAPPING INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was finished as follows unless otherwise noted:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (http://bacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: H_NH0811J09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://genome.wustl.edu/gsc
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                                                                                   /note="CpG_island (%GC=73.4, o/e=0.90, #CpGs=130)" 357. .360
/note="match to EST BE733203 (NID:g10147195)"
444. .573
                                                                                                                                                                                /note="match to EST AI066553 (NID:g3367255) co14g02.x1" 125. .1440
                                                                                                                                                                                                                                                                             1. .169
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                                                                                                                                                                                                                                                                                                             /note="match to EST BG777585 (NID:g14047902)"
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                                                                                                                                                                                                                                                                                                                                                                                                      note="match to EST AI830201 (NID:g5450861) wj78e05.x1"
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(NID:g16459189)"
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                                                                                        /note="similar to Mus musculus EST BB619995
                                                                                                                                                                           /note="match to EST AL556892 (NID:g12899973)"
                                                                                                                                                                                                                                                                                                                                                       (NID:g11616033)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="match to EST AL545268 (NID:g12877749)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="match to EST BI826228 (NID:g15937778)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NID:g13133998)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to Homo sapiens EST BG327560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="match to EST AA292501 (NID:g1940488) zt30b03.rl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="match to EST BI457310 (NID:g15247966)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rpt_family="GC_rich"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NID:g15938979)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NID:g15760344)"
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                                                                                                                                                                                                                                                                    /note="match to EST BI522595 (NID:g15347387)"
                                                                                                                                                                                                                                                                                                                                                                                                          note="similar to Homo sapiens EST BF528670"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="similar to Mus musculus EST AW229324 (NID:g6558620)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="match to EST BI833448 (NID:g15944998)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="match to EST BG831833 (NID:g14179420)"
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On May 30, 2000 this sequence version replaced gi:7023957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (18-FEB-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@sc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Only in DataBase (2000) In press (2000) 2 (bases 1 to 122717) 2 (bases 1 to 122717) 3 (bases 1 to 122717) 4 (bases 1 to 122717) 5 (bases 1 to 122717) 6 (bases 1 to 122717) 7 (bases 1 to 122717) 8 (bases 1 to 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 122,717 genomic DNA of 11q12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens chromosome 11 clone CMB9-83A3 map 11q12, WORKING DRAFT AP001186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                        Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 114906 bases at least Q40 Consensus quality: 11892 bases at least Q30 Consensus quality: 120476 bases at least Q20 Insert size: 121517; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                        Center project name: HumDraftll Center clone name: CMB9-83A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
    Quality coverage: 6.05x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center code: RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: RIKEN Genomic Sciences Center(GSC)
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960. .1143
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947. .1143
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(NID:914498907)"
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(NID:g15570185)"
1020. .1143
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1001. .1143
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Pred. No. 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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84154 92774: contig of 8621 bp in length
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18020 34939: contig of 16920 bp in length

34940 35039: gap of 100 bp

35040 49419: contig of 1380 bp in length
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                                                              63484.
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/note="assembly_fragment"
75237. .84053
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63484. .75136
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113210 contig of
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100657: contig of 7783 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               γυ3: gap of 100 bp 10.75136: contig of 11653 bp in length 236: gap of 100 bp 184053: contig of 8817 bp in length 153: gap of 100 bp 153: gap of 100 bp 153: gap of 1817 bp in length
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2002, 12:20:34; Search time 165.21 Seconds (without alignments) 31.223 Million cell updates/sec

Title: Perfect score:

Sequence: US-09-899-718A-3 21 1 agaaacaaacaaacaaacaaa 21

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	19.4		111	20 21 21 20 20 20 20 20 20 20 20 20 20 20 20 20	Score
92.4 92.4 92.4 92.4 92.4			95.29 95.29 95.22 22.22 444		Query
1355 1355 1355 1355	1140 1220 1300 1355	500 500 500 504	1265 1265 1646 500	2224 2224 11811 369 369	Length
2111	***		44444	4444	DB
US-08-442-282-4 US-08-442-282-16 US-08-442-281-4 US-08-442-281-16 US-08-939-727-4	-08-943-731-2 -09-227-357-5 -08-474-020A -07-757-390-4 -07-757-390-1	US-09-124-098-86 US-09-127-480-86 US-08-496-841C-86 US-09-328-111-120 US-09-328-141-120 US-09-306-042-2 US-09-306-042-2	-08-991 -09-062- -08-991 -09-062- -08-967- -08-592-	-08-477-347-2 -08-476-862-1 -09-078-294-7 -08-991-789A-19 -09-062-451-191	ID
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Sequence 3, Appli Sequence 1, Appli	32,	•	Sequence 32, Appl	Sequence 15, Appl	Sequence 2, Appli	Sequence 22, Appl	~	Sequence 1, Appli	Sequence 16, Appl						

ALIGNMENTS

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; NAME/KEY:
; LOCATION:
US-08-476-862-1
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                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 94039

FILING DATE: 06-APR-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 91229

FILING DATE: 06-AUG-1989

PRIOR APPLICATION DATA:
                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1847 AGAAACAAACAAACAAACAAA 1827
                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: WA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                 MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: THE INHIBITORS NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                               FILING DATE: 18-MAY-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: IL 1 FILING DATE: 12-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 0'CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/476,862 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                     LENGTH:
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BROWDY, Roger L.
25,618
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                                                                                                                                     2224 base pairs
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                                                                                      linear
                90..1472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.25
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                                                                                                    single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IL 107267
                                                                                                                                                                                                                                                                                                                                    IL 90339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6225054
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09078294 Patent No. 6265211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Du Sart, Desiree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: Davies Col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Choo, Kong-Hong Andy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3250 AGAAACAAACAAACAAA 3230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: BAC-F2 contig 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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                 REFERENCE/DOCKET NUMBER: 210121.419C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Frudakis, Tony N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                                           NAME: Potter, Jane E. R. REGISTRATION NUMBER: 33,332
                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                       APPLICATION NUMBER: US/08/991,789A FILING DATE: 11-Dec-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                 STATE: Washington
                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                         CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 701 Fifth Avenue, Suite 6300
TELEFAX: (206) 682-6031
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100.0%; Pred. No. 11;
tive 0; Mismatches
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RESULT 6
US-08-991-789A-169/c
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Best Local !
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APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Mak1, David J.
REGISTRATION UNMBER: 31,392
REFERENCE/DOCKET NUMBER: 21(
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                            148 AGAAACAAACAAACAA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 04-APR CLASSIFICATION:
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                                                                                                                                                                                                                                                                                    Local Similarity
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                      Conservative
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) 682-6031
NO: 191:
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100.0%; Pr
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100.0%; Pred. No
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Pred. No.
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; SEQUENCE DESCRIPTION: SEQ ID NO: 169: US-08-991-789A-169
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                                                                                                                                                                                                                                                                                                                                                    Sequence 169, Application US/09062451 Patent No. 6344550
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GENERAL INFORMATION:
APPLICANT: Frud
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                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: Fridakis, Tony l
APPLICANT: smith, John M.
APPLICANT: Reed, Steven G.
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ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                       TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             840 AGAAACAAACAAACAA 821
                                                                                                                                 STREET: 6300 C
                                                                                                                    STATE:
                                                                                              COUNTRY:
                                                                                                                                                                              ADDRESSEE:
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NAME: POTTET, Jane E. R. REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 210121.419C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,789A
FILING DATE: 11-Dec-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group
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TELEFAX: (206) 682-6031
                                                                                                                  Washington
                                                                                                                                                         6300 Columbia Center, 701 Fifth Avenue
                                                                                                  USA
                                                                                                                                                                                                                                                                                                                 Frudakis, Tony N.
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                         INFORMATION FOR SEQ ID NO: 290:
SEQUENCE CHARACTERISTICS:
LENGTH: 1646 base pairs
TYPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/991,789A
FILING DATE: 11-Dec-1997
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Frudakis, Tony N. Smith, John M. Reed, Steven G.
                                                                                                                                                                                             NAME: POTTET, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 210121.419C3
TELECOMUNICATION INFORMATION:
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                     SEQUENCE DESCRIPTION: SEQ ID NO: 290:
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                                     STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                           TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
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tive 0; Mismatc
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US-08-967-101-86
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Patent No.
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Best Local Similarity
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                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
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TELEFAX: (206) 682-60:
INFORMATION FOR SEQ ID NO:
APPLICANT: ST. GEURGE .... APPLICANT: ROMMENS, JOHANNA M APPLICANT: FRASER, PAUL E TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED TITLE OF INVENTION: TO ALZHEIMER'S DISEASE TITLE OF SEQUENCES: 183
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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CLASSIFICATION:
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100.0%; Pre
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100.0%; Pred. No.
tive 0; Mismatc
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24;
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CORRESPONDENCE ADDRESS:

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: PITCHET, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 86:
                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
NAME: Pitcher, Edmund R. TELECOMMUNICATION INFORMATION:
                 ATTORNEY/AGENT INFORMATION: NAME: Pitcher, Edmund R.
                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
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                                                                                                                                                                                                                                                        STREET: High
CITY: Boston
STATE: Massac
                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                     ZIP: 02110
                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 ACAAACAAACAAACAAACAAA 90
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CITY: Boston
                                                     CLASSIFICATION:
                                                                     FILING DATE:
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DEDNESS: single
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High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08592541
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High Street Tower - 125 High Street
                                                                                                                                                                                                                                    U.S.A.
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95.2%;
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Pred. No. 38
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SEQUENCE CHARACTERISTICS:

LENGTH: 500 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-592-541-86
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                           Qy
                                                                                                                                     ; STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) US-09-124-698-86
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                                                            Matches
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                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                            NAME: Pitcher, Edmund R. TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: CLASSIFICATION:
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70 ACAAACAAACAAACAAACAAA 90
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                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/124,698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
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                1 agaaacaaacaaacaaacaaa 21
                                                                          Local Similarity
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: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROMMENS, JOHANNA M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (617) 248-7000
(617) 248-7100
                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                       92.4%;
95.2%;
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95.2%;
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                                                                          Score 19.4;
Pred. No. 3
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Pred. No. 3
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                                                          Mismatches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617) 248-710
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES
TITLE OF INVENTION: TO ALZHEIMER'S DIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Pitcher, Edmund R. TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                           70 ACAAACAAACAAACAAA 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                           1 agaaacaaacaaacaaa 21
                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, PC
STREET: 805 Third Avenue
                                                                                                        TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                    Similarity
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STATE: New York COUNTRY: U.S.A.
                               CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: TESTA, HURWITZ & THIBEAULT
High Street Tower - 125 High :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: (617) 248-7000
(617) 248-7100
POR SEQ ID NO: 86:
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                                                                                                                                                                                                                                                                                                                                                                   Score 19.4;
Pred. No. 38;
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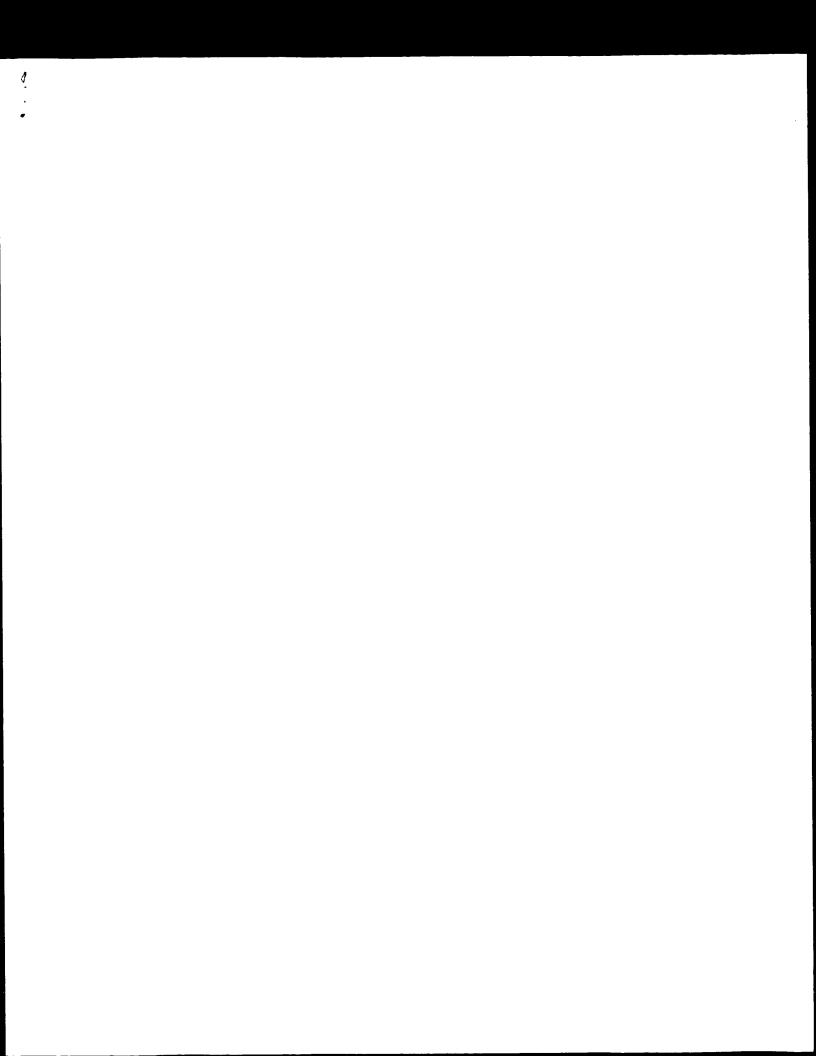
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APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-27 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER: OF SEQ ID NOS: 850
NAME/KEY: misc_feature; LOCATION: (1)...(504); OTHER INFORMATION: n = A,T,C US-09-328-111-120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-328-111-120/c
                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 120, Application US/09328111 Patent No. 6262333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Catino, Theo APPLICANT: Derti, Adnan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Burgess, Christopher APPLICANT: Bushnell, Steven E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ford, Donna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Carroll III, Eddie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Steinmann, Kathleen E. APPLICANT: Astle, Jon H.
                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Endege, Wilson O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 86:
                                                                                    FEATURE:
                                                                                                                                                      LENGTH: 504
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CLASSIFICATION: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Paul F. Fehlner, Ph.D.
REGISTRATION NUMBER: 35,135
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Catino, Theodore J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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95.2%; Pred. No. 38;
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Search completed: July 31, 2002, 12:20:35 Job time: 11658 sec



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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	
OM nucleic - nucleic search, using sw model	
Run on: July 31, 2002, 12:11:53; Search time 5855.71 Seconds (without alignments) 48.403 Million cell updates/sec	
Title: US-09-899-718A-3 Perfect score: 21 Sequence: 1 agaaacaaacaaacaaa 21	
Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	
Searched: 13736207 segs, 6748477542 residues	
Total number of hits satisfying chosen parameters: 27472414	
Minimum DB seq length: 0 Maximum DB seq length: 2000000000	
Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries	
Database: EST:* 1: em_estba:* 2: em_esthum:* 3: em_estin:* 4: em_estov:* 5: em_estvo:* 6: em_estvo:* 8: em_htc:* 9: gb_est:* 10: gb_est:* 11: gb_htc:* 12: gb_gss:* 13: em_gss_hum:* 14: em_gss_pln:* 15: em_gss_pln:*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	% Query Match Length DB	DВ	ID	Description
c 1	21	100.0	58	12	AZ504073	AZ504073 1M0344C07
N	21	100.0	100	10	BJ046075	•
ω	21	100.0	139	10	BG998551	
4	21	100.0	144	10	BI043282	
₅	21	100.0	148	9	AI345073	AI345073 tb62b07.x
ი 6	21	100.0	149	10	BF922085	BF922085 CM2-NT017
c 7	21	100.0	150	9	AA639520	AA639520 ng91a09.s
c 8	21	100.0	156	12	AZ493323	AZ493323 1M0327M24
9	21	100.0	156	12	BH105347	BH105347 RPCI-24-3
10	21	100.0	167	φ	AI253971	AI253971 qv54a05.x
11	21	100.0	167	9	AI733948	AI733948 qv54a05.x
12	21	100.0	177	9	AA719825	AA719825 zh39d02.s
c 13	21	100.0	180	9	AA457363	AA457363 aa91f12.r
14	21	100.0	181	ø	AI733998	AI733998 qv55g05.x
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16	21	100.0	187	9	AI251238	AI251238 qv55q05.x
c 17	21	100.0	187	9	AI792899	AI792899 qv55g05.y

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AII, AII, AII, AII, AII, AII, AII, AII,	
AZ656418 AI792857 AI792857 AAR839213 AAR839213 BB150403 BB536522 BE0711089 BB74727441 AV22747441 BAF2472441 AV264285 AZ21788 AZ221788 AZ221788 AZ221788 AZ221788 AZ21788 AZ21788 AZ21788 AZ21788 AZ21788 AZ21788 AZ21788 AZ21788 AZ21788 AZ21788 AZ21788 AZ21788 AZ217787 AZ414744 BE850705 AZ413748 BB425056 BB850705 AQ675544 AZ413748 AZ772597	
11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
A 152 A 152 A 164 A 177 A 184 A 184	
AZ6564 W 100531M AZ6564 V W 95309. AZ792857 QV54805. AAR39213 V W 95309. AAR39213 V W 95309. BA1465751 V W 95309. BB150403 BB150403 BB536522 BB536522 BB5071169 RC3 BF05 AV217088 AV317088 BB183787 BB183787 AV229441 AV229441 BF747295 RC1 - BT0 AV221788 RPC1 - BT0 AV261277 AV261267 AV230114 AV230114 BE852501 U W 21004 AV36257 AV264285	
694440 6978	
Wy54a05. W Wy5a09. x Gy54a05. y Wy5a09. r Wy5a09. r Wy5a09. r Wy5a09. r Wy5a09. r Wy5a09. r Wy5a09. r Wy5a09. r Wy5a62. r	
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ALIGNMENTS

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FEATURES Source	JOURNAL COMMENT	AUTHORS	VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE	RESULT 1 AZ504073/c LOCUS DEFINITION
Tel: 801 585 5606 reax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0344 row: C column: 07 Seq primer: CGTTGTANANCGACGGCCAGT Class: plasmid ends High quality sequence stop: 58. Location/Qualifiers 1. 58 /organism="Mus musculus" /strain="C57BL/6J" /clone="TUGCLM0344C07" /clone="TUGCLM0344C07" /clone="TUGCLM0344C07"	Unpublished (2000) Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.	AZ504073.1 GI:10685389 AZ504073.1 GI:10685389 GSS. house mouse. Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 58)	AZ504073 58 bp DNA linear GSS 05-OCT-2000 IM0344CO7F Mouse 10kb plasmid UUGCIM library Mus musculus genomic Clone UUGCIM0344CO7 F, DNA sequence.

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BASE COUNT
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Query Match
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                                                                                                                                                                                                                                                                                                                    source
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                                                                                                                                                                                                                                                                                                                                             Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
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BJ046075.1 GI:17398266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expressed genes in X. laevis embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopodinae; Xenopus.

1 (bases 1 to 100)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   African clawed frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    laevis cDNA clone XL006d02 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   musculus C57BL/6J (male) was obtained from the Jackson
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/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                            /tissue_type="whole embryo"
/dev_stage="stage 15"
                                                                                                                                                                                                                                       /clone="XL006d02"
                                                                                                                                                                                                                                                                   /db_xref="taxon:8355"
                                                                                                                                                                                                              /clone_lib="NIBB Mochii normalized Xenopus neurula
                                                                                                                                                                                                                                                                                           organism="Xenopus laevis"
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ORIGIN

RESULT

BI043282

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SOURCE

KEYWORDS VERSION ACCESSION

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This sequence was derived from the FAPESP/LICR Human Cancer Genome
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                                                                                                                                                                                                                               /note-"Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-1lbrary was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4st2=PM4-OT0201-
120301-001-d03_1&t3=2001-03-12&t4=1)
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                                                Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                         Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                 Contact: Simpson A.J.G
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National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jacobson, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CCAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                           Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Directionally cloned. Size-average insert size 500 bp. non-amplified. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oligodendroglioma tissue, cDNA made by oligo-d7 Directionally cloned. Size-selected on agarose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:2058901"
/clone_lib="NCI_CGAP_Brn20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: brain; Vector: pAMP1; mRNA made from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="oligodendroglioma"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-NT0170-
181100-536-e05&t3=2000-11_18&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                     www-bio.llnl.gov/bbrp/image/image.html
Seg primer: -40m13 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Preparation: M. Bento Soares, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 150)
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/note="Organ: colon; vector: p7773D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from RER+ colon tumor, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="Adult"
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                                                                                                            /tissue_type="colon tumor RER+"
/lab_host="DH10B"
                                                                                                                                                                 /clone_lib="NCI_CGAP_Co9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 156)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0327 row: M column: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606 Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
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and Wright,D.,Weiss,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse.
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                          musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              585 5606
                                                                                                                                                                                                                                                                                                                  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                               Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                              /note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                 /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="UUGC1M0327M24"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
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                                                                                                                                                                                                                        (http://www.jax.org/resources/documents/dnares/). The DNA
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Pred. No. 5.9e+04;
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    Best Local Similarity
                           Query Match
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library PRCI-24. For BAC
Library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
plate: 379 row: D column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Other_GSSs: RPCI-24-379D17.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levin Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E. Russell, D., de Jong, P. and Fraser, C.M. Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPCI-24-379D17.TJ RPCI-24 Mus musculus genomic clone RPCI-24-379D17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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                                                                                                                                                                /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1; RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the
                                                                                                                                                BamH1 sites using MboI
                                                                                                                                                                                                                                                                             /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-379D17"
/clone_lib="RPCI-24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                  /cell_type="Spleen/Brain"
/note="Vector: pTARBAC1;
                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
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Pred. No. 5.8e+04;
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                                                                                                                                              partially digested male C57BL/6J
                    DB 12;
  .8e+04;
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                  Length 156;
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TITLE
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                                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue procurement: W. Marston Linehan, M.D., Rodrigo F. Chuaqui,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium, LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llni.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco.
                                         Homo sapiens
                                                                               EST
                                                                                                                              qv54a05.x5 NCI_CGAP_Ov32 Homo mRNA sequence.
     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                    AI733948
                                                                                            AI733948.1
                                                              numan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: ovary; Vector: pAMP1; mRNA made from ovarian carcinoma, cDNA made by oligo-dT priming.
Non-directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Non-amplified library. "
23 c 31 g 34 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1985360"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="papillary serous carcinoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="NCI_CGAP_Ov32"
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Primates;
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Pred. No. 5.6e+04;
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sapiens cDNA clone IMAGE:1985360 3',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 agaaacaaacaaacaaacaaa 21
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Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuaqui,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Dental Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Original clone citation: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
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                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                           Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                               Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                         Contact: Wilson RK
                                                                                                                               Unpublished (1997
                                                                                                                                                           White,Y., Wylie,T., Waterst
WashU-NCI human EST Project
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314 286 1800
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Non-directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Non-amplified library.

a 23 c 31 g 34 t
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Pred. No. 5.6e+04;
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180 bp mRNA linear EST 06-JUN-199
aa91f12.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone
IMAGE:838703 5' similar to contains element MER22 repetitive
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 180)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Hillier,L., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.
Kucaba,T., Lacy,M., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,
Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,
T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the rMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev1 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WashU-Merck EST Project 1997
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                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
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/lab_host="DH10B (ampicillin resistant)"
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/db_xref="GDB:1319706"
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                        /clone_lib="Stratagene fetal retina 937202"
/sex="mixed"
                                                                    /clone="IMAGE:838703"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                             Location/Qualifiers
                                                                                             /db_xref="taxon:9606"
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100.0%; Pred. No. 5.4e+04;
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1 (Dases 1 to 181)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This read is a RESEQUENCE of a previously sequenced human clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insert Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI733998.1 GI:5055111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
           Conservative
                                                                                                                                               78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              orientation)
Length: 238
                                                                                                                                   /note="Organ: ovary; Vector: pAMP1; mRNA made from ovarian carcinoma, cDNA made by oligo-dT priming.

Non-directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Non-amplified library. "

32 c 34 g 37 t
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                                                                                                                                                                                                                                                    /tissue_type="papillary serous carcinoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:1985528"
/clone_lib="NCI_CGAP_Ov32"
                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                   /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           -40UP from Gibco
                         100.0%; Score 21; 1
100.0%; Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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Pred. No. 5.4e+04;
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                                                 DB 9;
                         .4e+04;
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FEATURES
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BB072882/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   trehalose and its application for the synthesis of full length CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 10-14, 10-16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci.p., Nishiyama.y., Westover.A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki.y.
Thermostabilization and thermoactivation of thermoalabile enzymes by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BB072882 RIKEN full-length enriched, adult male colon M cDNA clone 9030619B06 3' similar to U43144 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        further details
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 184)
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BB072882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      visit our web site (http://genome.rtc.riken.go.jp) for
                         prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
   Genomic Sciences Center and
                                                                                                /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="9030619B06"
                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus'
/strain="C57BL/6J"
                                                                                                                                        /lab_host="DH10B"
                                                                                                                                                                    /dev_stage="adult"
                                                                                                                                                                                                            /tissue_type="colon"
                                                                                                                                                                                                                                                                 /clone_lib="RIKEN full-length enriched, adult male colon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
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Search completed: July 31, 2002, 12:11:57 Job time: 13470 sec
                                                                Query Match 100.0%; Score 21; DB 9; Length 184; Best Local Similarity 100.0%; Pred. No. 5.3e+04; Matches 21; Conservative 0; Mismatches 0; Indels
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1: \SIDSI\gcgdata\hold-geneseq\geneseqn-embl\Nal980.DAT: *
2: \SIDSI\gcgdata\hold-geneseq\geneseqn-embl\Nal981.DAT: *
3: \SIDSI\gcgdata\hold-geneseq\geneseqn-embl\Nal981.DAT: *
3: \SIDSI\gcgdata\hold-geneseq\geneseqn-embl\Nal981.DAT: *
4: \SIDSI\gcgdata\hold-geneseq\geneseqn-embl\Nal981.DAT: *
4: \SIDSI\gcgdata\hold-geneseq\geneseqn-embl\Nal981.DAT: *
5: \SIDSI\gcgdata\hold-geneseq\geneseqn-embl\Nal981.DAT: *
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7: \SIDSI\gcgdata\hold-geneseq\geneseqn-embl\Nal99.DAT: *
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                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
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Result	Score	Query Match Length DB	Length		ID
c 1	21	100.0	35	18	AAT93839
N	21	100.0	140	21	AAC13041
ω	21	100.0	384	20	AAV87203
4	21	100.0	770	21	AAC44102
U	21	100.0	1106	22	AAS46192
σ	21	100.0	1122	22	AAD09952
c 7	21	100.0	1409	22	ABA16382
8	21	100.0	1688	21	AAC79000
c 9	21	100.0	2224	16	AAQ89544

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22	22	2 2) V) K	2 0	22	22	22	22																									
AAK89370	AAK81009	AAK81266	AAS20/24	AA167272	AAI67271	AAK81010	AAK70316	AAK70315	AAK70314	AAV83943	AAK89493	AAK74469	AAK89492	AAK74467	ABI99827	AAL04707	AAK51993	AAS84690	AAI60242	AAK53345	AAI58456	AAK52361	ABL26224	AAH51796	AAA49207	AAH15452	AAC83951	AAQ10907	AAK85886	AAK85885	AAK85884	AAH48860	AAZ09171	AAQ10956
Human digestive sy			Human genomic DNA		Human FK506-bindin					Bacterial artifici	dianetino a		dimestive s	3 (ischaemic		Human polynucleoti	avodina nove	Human polynucleoti	polymucleot			Drosophila melanoc	ir necr			40	-3	Human immune/haema				=	Encodes himan 75kn

ALIGNMENTS

PA PI	PR XX	XX	YY DD	X P X	Y F F		20	XXX	KW	XX	X D	X A	RESULT AAT938 ID A
(SAIC-) SAICOM SRL. Quadrifoglio F, Scaggiante B;	04-DEC-1995; 95IT-0MI2539.	04-DEC-1996; 96WO-EP05388.	12-JUN-1997.	WO9720924-A1.	<pre>/*tag= a /note= "phosphodiester oligonucleotide"</pre>	modified_base 135	Synthetic.	tumoural cell line; cytotoxic activity; tumour cell; lymphoma; lymphoblastic tumour; ss.	Phosphodiester; selective binding; cell viability; growth;	Phosphodiester oligonucleotide 29 with cytotoxic activity.	24-FEB-1998 (first entry)	AAT93839;	RESULT 1 AAT93839/c ID AAT93839 standard; DNA; 35 BP.

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RESULT
AAC13041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The oligonucleotides (see also AAT93811-27) are believed to selectively bind and sequester some proteins which are essential to the viability bind and sequester some proteins which are essential to the viability and growth of tumoural cell lines. They have specific and selective cytotoxic activity against tumour cells, and can be used for treating tumours of the liquid type, in particular of lymphoblastic origin, and of the solid type, in particular lymphomas. Oligonucleotides AAT93834-36 were created to determine the relevance of the specific features of the above generic formula, in determining cytotoxic activity. The present sequence is different from the generic sequence in that the sequence has flanking fragments containing C and T bases. The results showed that sequences having flanking fragments containing C and T bases do not exert any significant activity activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel phosphodiesteric oligonucleotides AAF93837-41 are based on the generic formula, in the 3'-5' or 5'-3' direction:

(GaTa')a''-(GbTb')b''-(GcTc')c''-(GdTd')d''-(GeTe')e''-(GfTf')f''-

(G-Tg')g''.N', where:

N and N' = T or G, equal or different from each other;

x = 0-8, equal or different from each other;

a', b', c', d', e', f', and g' = 0-10, equal or different from each other;

a', b', c', d', e', f', and g' = 0-30, equal or different from each other.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New phospho:di:esteric oligo:nucleotide(s) - which exert a specific and selective cytotoxic effect on tumour cells, for treating both solld and liquid tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 5; Page 12; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-319771/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       other;
                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            any significant cytotoxic activities
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                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC13041 standard; cDNA; 140 BP
                                                                                                                                                                                                                                                                                              Human;
                                                                                                                                                                                                                                                                                                                             Human secreted protein 5' EST, SEQ ID NO: 17116.
                                                                                                                                                                                                                                                                                                                                                                 06-OCT-2000
                                                                                                                                                                                                         EP1033401-A2
WPI; 2000-500381/45
                                  Dumas Milne Edwards J,
                                                                 (GEST ) GENSET
                                                                                                                                    21-FEB-2000; 2000EP-0200610
                                                                                                                                                                      06-SEP-2000
                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 AGAAACAAACAAACAAA 11
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                                                                                                                                                                                                                                                                          therapy;
                                                                                                                                                                                                                                                                                            5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                            chromosome mapping; ss
                                                                                                     99US-0122487
                                                                                                                                                                                                                                                                                            expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                    Duclert A,
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Pred. No. 1.3e+02;
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                                      Giordano J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 140 BP; 47 A; 38 C; 38 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is one of a large number of 5' ESTs derived from
                                                                                                                                                                                                                                                                                                                                                                                                                           Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; h chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                              W09845435-A2
                                                                                                                                                                                                                                                                                                                                                                                                            receptor; ligand; anti-inflammatory; tumour inhibitor; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV87203;
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                                                                                                                                                                                                                                               10-APR-1997;
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                                                                                                                                WPI; 1999-070076/06.
                                                                                                                                                                                 Agostino MJ,
                                                                                                                                                                                                                                                                               10-APR-1998;
                                                                                                                                                                                                                                                                                                                15-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 agaaacaaacaaacaaacaaa 129
                                                                              New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain,
                                                                                                                                                              Racie LA,
                                                                                                                                                                                                              (GEMY ) GENETICS INST INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID 17116; 71pp + CD-ROM; English.
                                                                                                                                                              J, Jacobs K,
Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       human;
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This sequence represents an expressed sequence tag (EST), and is

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Page 487; 633pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and include nutritional activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activiny, neceptor/ligand activity, haematory activity, cacherin/tumour invasion suppressor activity, tumour inhibition activity, receptor/ligand activity, anti-inflammatory activity, cacherin/tumour invasion suppressor activity, tumour inhibition activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                          06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana DNA fragment SEQ ID NO: 41638.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC44102 standard; DNA; 770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  384 BP; 89 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                          2000EP-0301439
           99US-0121825-
99US-0123180-
99US-0125788-
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99US-0132486-
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99US-0139453
99US-0149433
99US-0149484
99US-0144333
99US-0145086
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990S-0145913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; col adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disord PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS46192
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Similarity 100.
21; Conservative
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             2000WO-USO5601.
2000WS-IB720ZP.
2000US-IB932DP.
2000US-IB932DP.
2000US-IB932DP.
2000US-IB932DP.
2000WO-USO68B4.
2000US-I9104BP.
2000US-I9104BP.
2000US-I9104BP.
2000US-I9104BP.
2000US-I93053P.
2000US-I93053P.
2000US-I93053P.
2000US-I9444P.
2000US-I9444P.
2000US-I95075P.
2000US-I95075P.
2000US-I9682DP.
2000US-I9682DP.
2000US-I9682DP.
2000US-I9682DP.
2000US-I9682DP.
2000US-I9682DP.
2000US-I9682DP.
2000US-I99550P.
2000US-I99550P.
2000US-USI3705.
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99US-0161406.
99US-0161359.
99US-0161360.
99US-0161361.
99US-0161920.
99US-0161992.
99US-0161993.
99US-0161993.
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Pred. No. 1.2e+02;
); Mismatches 0;
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colon; SS

27-JUL-1999;
27-JUL-1999;
27-JUL-1999;
28-JUL-1999;
28-JUL-1999;
20-AUG-1999;
20-AUG-1999;
20-AUG-1999;
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20-AUG-1999;
20-AUG-1999;
20-AUG-1999;
21-AUG-1999;
22-AUG-1999;
22-AUG-1999;
23-AUG-1999;
24-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                Human; drug metabolising enzyme; DME-17; immunosuppressive; gene therapy; cytostatic; autoimmune disorder; inflammatory disorder; atherosclerosis; osteoporosis; eye disorder; hepatic tumour; Addison's disease; cretinism; rheumatoid arthritis; acquired immune deficiency syndrome; AIDS; anaemia; developmental disorder; endocrine disorder; iritis; acromegaly; epilepsy; thyrotoxicosis; pancreatic disorder; diabetes mellitus; obesity; adenoma; gastrointestinal disorder; nodular hyperplasia; conjunctivitis; glaucoma; actinic keratosis; metabolic disorder; dysphagia; anorexia; carcinoma;
                                                                                                                                                                                     Human drug metabolising enzyme (DME-17) cDNA.
                                                                                                                                                                                                                          12-SEP-2001 (first entry)
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02-JUN-2000;
05-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                         845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals and to screen for modulators of the compounds -
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08-NOV-2000;
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22-AUG-2000;
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Smith V, W
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2000WO-US15264.
2000WS-209832P.
2000WO-US20710.
2000WS-0644848.
2000WO-US23328.
2000WO-US33678.
2000WO-US33678.
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Pred. No. 1.1e+02;
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В
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CC Human DME and its nucleic acid molecule are useful for the diagnosis,
CC treatment and prevention of disorders associated with increased or
CC decreased expression of DME. Examples of such disorders include,
CC autoimmune/inflammatory disorder such as acquired immune deficiency
CC syndrome (AIDS), rheumatoid arthritis, osteoporosis; cell proliferative
CC disorder such as actinic keratosis, atherosclerosis; developmental
CC disorder such as epilepsy, anaemia; endocrine disorder such as
CC disorder such as epilepsy, anaemia; pancreatic disorder such as
CC disorder such as epilepsy, anaemia; pancreatic disorder such as
CC diabetes mellitus; eye disorder such as conjunctivitis, glaucoma, iritis;
CC disorder such as anorexia, dysphagia and hepatic tumours including
CC metabolic disorder such as Addison's disease, obesity; gastrointestinal
CC disorder such as anorexia, dysphagia and hepatic tumours including
CC modular hyperplasia, adenomas and carcinomas. DME DNA is useful for
CC creating 'Knockin' humanised animals (pigs) or transgenic animals (mice
CC or rats) to model human disease. DME DNA is also in useful is gene
CC therapy. DME and its immunogenic fragments are useful for screening
                                                           Matches
                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drug metabolizing enzymes and encoding polynucleotides, useful for diagnosing, treating and/or preventing autoimmune, inflammatory, coproliferative, developmental, endocrine, eye, metabolic, and
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Ring HZ,
                                                                                                                               Sequence 1122 BP; 338 A; 228 C; 261 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                gastrointestinal disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-425874/45
    845
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21-JAN-2000;
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              1 agaaacaaacaaacaaa 21
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                                                           21;
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, Hillman JL,
DB, Tang YT,
                                                                                                                                                        of compounds in several drug screening assays.
                                                          Conservative
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2000US-0177443.
2000US-0178574.
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213..752
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123..212
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                                                                      Score 21;
Pred. No.
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                                                        Mismatches
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                                                                                     21;
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                                                                   1.1e+02;
                                                                                   DB 22;
                                                                                                                               T; 0 other;
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                                                                                   Length 1122;
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ABA16382,

ABA16382 standard; DNA; 1409 BP

ABA16382;

RESULT

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18-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
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26-JUL-2000;
26-JUL-2000;
14-AUG-2000)
14-AUG-2000;
12-AUG-2000;
12-AUG-2000;
13-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
16-AUG-2000;
17-AUG-2000;
18-AUG-2000;
18-AUG-2000;
18-AUG-2000;
19-AUG-2000;
19-AUG-2000;
19-AUG-2000;
10-SEP-2000;
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2000US-0184664

2000US-0184664

2000US-0186350

2000US-0198074

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2000US-0198123

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2000US-0218890

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                                                2000US-0225447.
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2000US-0225266.
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2000US-0231244.
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2000US-0231414.
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2000US-0231414.
2000US-0232080.
2000US-0232081.
2000US-0231968.
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            21-SEP-2000;
21-SEP-2000;
25-SEP-2000;
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26-SEP-2000;
27-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
03-OCT-2000;
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08-NOV-2000;
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2000US-0232398.
2000US-0232400.
2000US-0232401.
2000US-0233063.
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2000US-0234223.
2000US-0234223.
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2000US-0234234.
2000US-023434.
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2000US-0241785.
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2000US-0241808.
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2000US-024617

2000US-0246475

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2000US-0236327.
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2000US-0246527.
2000US-0246528.
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2000US-0239937.
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                                                                                                                                                                                                                                                                                   AAC79000
                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel genes (ABA11004-ABA21534) and proteins CC (ABB14678-ABB18001) useful for preventing, treating or ameliorating cmedical conditions e.g. by protein or gene therapy. The genes are CC isolated from a range of human tissues disclosed in the specification. CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast CC and ovarian cancer and other cancers of the adrenal gland, bone, bone cancer and other cancers of the adrenal gland, bone, bone conditions, breast, gastrointestinal tract, liver, lung, or urogenital; chaemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (c) cardiovascular disorders such as myocardial ischaemias; (c) cardiovascular disorders such as myocardial ischaemias; (c) cardiovascular disorders such as viral, bacterial, fungal CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal CC entry are sequence data for this patent did not form part of the CC printed specification, but was obtained in electronic format directly crom wipo at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                 Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticorulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiavascular disorden; neurological disease; infection; human; secreted protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
                                                                                                                                                Human secreted protein gene 4 clone HCEGS49.
                                                                                                                                                                                                                                                           AAC79000 standard; DNA; 1688 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1409 BP; 361 A; 334 C; 324 G; 390 T; 0 other;
           Homo sapiens
                                                                                                                                                                                           14-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-DEC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 8713; 1701pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancers and metastases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                   676 AGAAACAAACAAACAAA 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; 2000US-0251030.
2000US-0251988.
2000US-0256719.
2000US-0251479.
2000US-0251856.
2000US-0251868.
2000US-0251869.
2000US-0251999.
2000US-0251990.
2000US-0254097.
2001US-0254097.
                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 21; DB 22;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                      cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1409;
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AAQ89544/c
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                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local (
                                                                                     Homo sapiens
                                                                                                                                                              p75 Tumour Necrosis Factor Receptor.
                                                                                                                                                                                                   31-OCT-1995 (first entry)
                                                                                                                                                                                                                                      AAQ89544;
                                                                                                                                                                                                                                                                    AAQ89544 standard; DNA; 2224 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                                                                                                                     receptor; ss.
                                                                                                                               Ligand; tumour necrosis factor; nerve growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1688 BP; 516 A; 310 C; 384 G; 478 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 317; 367pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful in the prevention, treatment and diagnosis of cancer, disorders, cardiovascular disorders and neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fourty nine nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAR-1999;
14-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                    1 agaaacaaacaaacaaa 21
                                                                                                                                                                                                                                                                                                                                                                         21;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                  Location/Qualifiers 90..1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0126602
/product= p75 TNF receptor.
                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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/transl_except= CCA misc_difference 1146..1148
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misc_difference 1170..1172
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misc_difference 1188..1190
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                                                                                                                                                                                        /transl_except= GAT encodes Glycine.misc_difference 1197..1199
                                                                                                                                                                                                                       /transl_except= TCA encodes Histidine misc_difference 1194..1196
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misc_difference 2003..2005
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misc_difference 2000..2002
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                       misc_difference
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1140..1142
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1149..1151
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1161..1163
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1158..1160
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1155..1157
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1152..1154
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1191..1193
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1176..1178
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1173..1175
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1167..1169
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1182..1184
                                                 /transl_except=
2017..2018
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2015..2016
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2012..2014
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2006..2008
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                         /transl_except=
2019..2021
          /transl_except=
                   /*tag=
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                                                                                                                                                                                                                                                          AGC encodes Glycine
                                                                                                                                                                                                                                                                                  ACC
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                                                                                                                                  CCT
                                                                                                                                                                                    TCT
                                                                                                                                                                                                                                                                                                           GCC encodes
          CAG
                                                                                   CAT
                                                                                                           GGT encodes Proline
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                                                          GGG
                                  ACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encodes Arginine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         encodes Alanine
                                                                                                                                                                                                                                                                                                                                 encodes Aspartic acid
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                                                                                                                                                                                                                                                                                  encodes Proline
                                                                                                                                   encodes Alanine
                                                                                                                                                                                   encodes Threonine
          encodes
                                                          encodes Glutamic acid.
                                                                                   encodes Valine
                                   encodes
                                                                                                                                                                                                                                                                                                                                                           Serine
                                                                                                                                                                                                                                                                                                           Serine
            Serine
                                    Alanine
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AAQ10956/c
ID AAQ109
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A ligand to a member of the tumour necrosis factor (TNF)/nerve growth factor (NGF) receptor family which binds either to the region of the 4th-Cys rich domain of the receptor, or to the region between it and the cell membrane may be used in the production of a pharmaceutical composition for increasing the inhibitory effect of a soluble receptor of the TNF/NGF receptor family. This sequence encodes the p75 TNF receptor. N in the sequence represents an unidentified nucleotide (poor reproduction in specification).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP648783-A.
                                                                                                                                                                                                                                                                                                                                                       Sequence 2224 BP; 432 A; 697 C; 688 G; 400 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Figure 2; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumour necrosis factor (TNF) receptor ligand - used inhibitory effect of a soluble TNF receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-148673/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (YEDA ) YEDA RES & DEV CO LTD. (WALL/) WALLACH D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-OCT-1993;
                                       20-APR-1990;
12-SEP-1989;
08-MAR-1990;
                                                                                                                                                                                                    autoimmune glomerulonephritis; lymphokine; cytokine.
                                                                                                                                                                                                                Tumour Necrosis Factor; binding proteins; septic shock;
                                                                                                                                                                                                                                                                                  AAQ10956;
                                                                                                                                                                                                                                                                                                     AAQ10956 standard;
                                                                                                                                                                                                                                      Encodes human 75kD TNF-binding protein.
                                                                                                                                                                                                                                                            24-MAY-1991
Brockhaus M,
                                                                                     31-AUG-1990;
                                                                                                         20-MAR-1991.
                                                                                                                              EP417563-A.
                    (HOFF ) HOFFMANN-LA ROCHE AG
                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                             (first entry)
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 Dembic Z,
                                          90CH-0001347.
89CH-0003319.
90CH-0000746.
                                                                                      90EP-0116707
                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                   /product=
                                                                                                                                                                                                                                                                                                      DNA; 2339
                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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   Gentz
                                                                                                                                                      75kD TNF-BP
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Pred. No. 1.1e+02;
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  Lesslauer W,
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2224;
    Lotscher H;
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AAZ09171
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Best Local
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                                                              20-APR-1990;
12-SEP-1989;
08-MAR-1990;
Brockhaus M,
Schlaeger E;
                                                                                                                  31-AUG-1990;
                                                                                                                                              01-SEP-1999.
                                                                                                                                                                                                                                                                                                            Tumour necrosis factor binding protein; TNF; insoluble protein; agonist; anti-inflammatory; antimalarial; treatment; septic shock; inflammation; autoimmune glomerulonephritis; cerebral malaria; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Partial amino acid sequences were determined for the 55 and 75kD TNNF-BPS (see AARI1072-R11081) and oligonucleotide primers were synthesised based on these partial sequences. The primers were used to produce a cDNA fragment for use as aprobe to screen a human placental cDNA bank constructed in lambda gtll. Positive clones were identifed and sequencea. Repeated sequencing showed a discrepancy at position 7 such that the third codon encodes either Thr or Ser. DNA constructs comprising the TNF-BP coding sequence may also contain a fragment encoding a human Ig domain. Recombinant constructs are used to transform cells to confer improved TNF-
                                    (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                               Human tumour necrosis factor binding protein cDNA fragment.
                                                                                                                                                                                                                                                                                                       antagonist; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ09171 standard; cDNA; 2339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2339 BP; 494 A; 720 C; 685 G; 439
                                                                                                                                                                                                                                                                                                                                                                                                18-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insoluble tumour necrosis factor binding proteins - and DNA encoding them, useful in pharmaceutical prods. and for antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     See also AAQ10955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             binding properties.
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            Dembic
                                                              90CH-0001347.
89CH-0003319.
90CH-0000746.
                                                                                                                 90EP-0116707
                                                                                                                                                                                            /"cag" a
/product= "TNF binding protein"
/note= "Partial second-
                                                                                                                                                                                                                                      Location/Qualifiers
1..1179
           2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                        "Partial sequence, no start codon given"
                                                                                                                                                                                                                                                                                                        ds.
         Gentz R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No. 1.1
0; Mismatches
        Lesslauer
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        Loetscher
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Best Local Similarity
                                                                                         08-MAR-1990;
20-APR-1990;
31-AUG-1990;
31-AUG-1990;
WPI; 2001-559312/63
                        Brockhaus M,
Schlaeger E;
                                                                                                                                                12-SEP-1989;
                                                                                                                                                                          31-AUG-1990;
                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                 TNF; tumor necrosis factor binding protein; TNFBP; treatment; insoluble protein; antiinflammatory; immunosuppressive; antibacterial; antiprotozoal; treatment; meningococcal sepsis; cerebral malaria; autoimmune glomerulonephritis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel homogeneous insoluble proteins (I), their (in)soluble fragments (Ia) and their salts that can bind tumour necrosis factor (TNF). The products of the invention have anti-inflammatory and antimalarial activity (I) and (Ia) are used (i) to treat diseases in which TNF is involved (e.g. septic shock, autoimmune glomerulonephritis, cerebral malaria, immune responses and inflammation), (ii) to purify TNF; (iii) to identify TNF (ant)syonists and (iv) for diagnostic determination of TNF in body fluids. Antibodies raised against a tumour necrosis factor binding protein fragment described in the method of the invention.
                                                              (HOFF ) HOFFMANN LA ROCHE & CO AG
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                                                                                                                                                                                                                                                                                                                              Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New insoluble proteins, and fragments, that bind to tumor necrosis
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P-PSDB; AAY30935.
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                                      Dembic
                                                                                                                 89CH-0003319.
90CH-0000746.
90CH-0001347.
                                                                                        90EP-0116707
99EP-0100703
                                                                                                                                                                                                                                                     /product= "TNFBP-associated protein"
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100.0%; Pred.
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                                    Lesslauer W,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New homogeneous, insoluble proteins that bind tumor necrosis factor (TNF), useful for treating TNF-mediated disorders, e.g. inflammation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40696.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; gene therapy; vaccine; metastasis; ds.
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07-JUL-2000;
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30-JUN-2000;
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17-MAR-2000;
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             2000US-0216647

2000US-0217487

2000US-0217487

2000US-0217497

2000US-0218290

2000US-020963

2000US-022964

2000US-0224518

2000US-0224519
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2000US-0184664.
2000US-0186350.
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2000US-0198123.
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12-SEP-2000;
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27-SEP-2000;

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2000US-0226868.
2000US-0227182.
2000US-0227009.
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2000US-0225266.
2000US-0225267.
2000US-0225268.
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2000US-0231244.
2000US-0231413.
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2000US-0231968.
2000US-0232397.
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2000US-0232399.
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2000US-0234998.
2000US-0235484.
       2000US-0241826.
2000US-024617.
2000US-0246474.
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Barash SC, SM;

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 40696; 3071pp + Sequence Listing; English

cc amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cc activity, and can be used in gene therapy and vaccine production. (I) cc proteins and polynucleotides may be used in the prevention, diagnosis and cc treatment of diseases associated with inappropriate (I) expression. For cc example, they may be used to treat disorders associated with decreased cc expression by rectifying mutations or deletions in a patient's genome cc that affect the activity of (I) by expressing inactive proteins or to cc supplement the patients own production of (I). Additionally, (I) cc polynucleotides may be used to produce the secreted (I), by inserting cc the nucleic acids into a host cell and culturing the cell to express the cc diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic dartied genomic concerns the present inwannimune/haematopoietic antigen genomic concerns accommended to the protection. AK64703 to AAK67694 represent invention. AK54942 to AAK54950 and AAM82169 represent in the averantification of the present invention. sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

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04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2357 BP; 677 A; 465 C;
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17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; gene therapy; vaccine; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAK85885;
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                 2000US-0228924.
2000US-0229287.
2000US-0229343.
                                           2000US-0229467

2000US-0215135

2000US-0215647

2000US-0215647

2000US-0217486

2000US-0217496

2000US-0217496

2000US-0217496

2000US-022964

2000US-022964

2000US-0224518

2000US-0225214

2000US-0225214

2000US-0225214

2000US-0225266

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2000US-0227009
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2000US-0184664.
2000US-0186350.
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2000US-0205515.
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PR 05-SEP-2000; 2000US-022959; PR 16-SEP-2000; 2000US-022959; PR 16-SEP-2000; 2000US-0229513; PR 06-SEP-2000; 2000US-0211443.

PR 06-SEP-2000; 2000US-0211444.

PR 16-SEP-2000; 2000US-0211444.

PR 16-SEP-2000; 2000US-0211444.

PR 16-SEP-2000; 2000US-0211444.

PR 16-SEP-2000; 2000US-0212409.

PR 26-SEP-2000; 2000US-0212609.

PR 26
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AAK85886;

07-NOV-2001

(first entry)

AAK85886/c

AAK85886 standard; DNA; 2358 BP

RESULT

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В

427 AGAAACAAACAAACAAACAAA 407

1 agaaacaaacaaacaaa 21

Matches

21;

Conservative

0;

Score 21; DB 22; Pred. No. 1.1e+02;); Mismatches 0;

Length 2358; Indels 0

0; Gaps

0;

Query Match 100.0%; Best Local Similarity 100.0%;

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17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
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06-DEC-2000;
06-DEC-2000;
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08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                       AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynuclectides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, although the contract immune/haematopoietic related diseases, especially and contract immune/haematopoietic related diseases.
                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding human immune/hematopoietic antigen polypeptides. useful for preventing, diagnosing and/or treating cancers and metastasis -
Sequence 2358 BP; 679 A; 467 C; 345 G; 867 T; 0 other;
                                    represent sequences used in the exemplification of the present invention.
                                                     to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169
                                                                                        cancers and cancer metastases of haematopoietic derived cells. AAK64703
                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                            metastasis
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2000US-0249217.
2000US-0249218.
2000US-0249214.
2000US-0249244.
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2000US-0249299.
2000US-0249300.
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2000US-0251479.

2000US-0251856.

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2000US-0251988.
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Human immune/h Human; immune/h Human; immune; cytostatic; ge Homo sapiens. W0200157182-A2 09-AUG-2001. 17-JAN-2001; 2: 31-JAN-2000; 2: 02-MAR-2000; 2: 16-MAR-2000; 2: 17-MAR-2000; 2: 11-JUL-2000; 2: 11-J
Immune, haematopoletic antigen genomic sequence SEQ ID NO:40698. atic; gene therapy; vaccine; metastasis; ds. aplans.
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14-SEP-2000, 21-SEP-2000, 25-SEP-2000, 25-SEP-2000, 26-SEP-2000, 27-SEP-2000, 27-SE
2000US-0234934 2000US-0234274 2000US-0234274 2000US-0234997 2000US-0234997 2000US-0234997 2000US-0235836 2000US-0235836 2000US-0236368 2000US-0236368 2000US-0236368 2000US-0236368 2000US-0236368 2000US-0236368 2000US-0236368 2000US-0241785 2000US-0241785 2000US-0241786 2000US-0241786 2000US-0241786 2000US-0241809 2000US-0241809 2000US-024677 2000US-0246610 2000US-0246611 2000US-0246612 2000US-0246612 2000US-0246612 2000US-0246776 2000US-0246776 2000US-0246776 2000US-0246776 2000US-0246776 2000US-0246776 2000US-0246776 2000US-0249216 2000US-0259216 2000US-0250316 2000US-0251856

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                                                                                                                                                                                                                                  expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I). by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. ARK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased example,
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08-DEC-2000; 2000US-0251990.

11-DEC-2000; 2000US-0254097.

05-JAN-2001; 2001US-0259678.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
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427 AGAAACAAACAAACAAACAAA 407
                                                                                                           Match 100.0%; Score 21; DB 22; Length 2358; Local Similarity 100.0%; Pred. No. 1.1e+02;
                       1 agaaacaaacaaacaaa 21
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Search completed: July 31, 2002, 14:11:11 Job time: 17368 sec

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Post-processing: Minimum Match 0%
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AR152033 Sequence
A78517 Sequence 1
A26415 cDNA fragme
X03210 Mouse MHC Q
M55994 Human tumor
AK021890 Homo sapi
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AJ276965 Phycomyce
AJ278287 Phycomyce
G26865 human STS S
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G35045 STS NRU3-14
AU026129 Rattus no
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AX348020 Sequence
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ALIGNMENTS

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Sequence 3 from Patent WO0202785.
AX349065
AX349065.1 GI:18615100
                                                                                             Sprunck, S. Kluth, A., Becker, D., Luetticke, S. and Loerz, H. Promoters of gene expression in plant caryopses Patent: WO 02027/85-A 3 10-7AN-2002; Aventis CropScience GmbH (DE)
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                       /organism="synthetic construct"
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U76839
1 (bases 1 to 120)
Brockmann, B., Schnieders, F.,
DNA sequence divergence in a
and Apodemus flavicollis
Unpublished
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (01-NOV-1996) Max-Planck-Group, MDC for Molecular
Medicine, Robert-Rossle-Str. 10, Berlin-Buch 13125, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
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Mammalia; Eutheria;
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                                                                                                                                                                             Rattus norvegicus cyclin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brockmann, B., Schnieders, F., Kunze, B., Krawczak, M. and Schmidtke, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                          U76839.1 GI:2443416
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                                                                 Rattus
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80. .116
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Rattus norvegicus"
/db_xref="taxon:10116"
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Rodentia;
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Pred. No.
                                                                                                                                                                                                                                                                                                        Score 21; DB 10;
Pred. No. 2.5e+02;
Mismatches 0;
                                                                                                                                                                             120 bp
A gene,
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                          Kunze,B., Krawczak,M. and Schmidtke,J.
cyclin A gene of Apodemus sylvaticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
                                                                           Craniata; Vertebrata; I
Sciurognathi; Muridae;
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3e+02;
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                                                                             Euteleostomi;
; Murinae;
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             Query Match
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Direct Submission
Submitted (10-JAN-2001) Genomics, Monsanto, 800 North Lindbergh
Blvd., Creve Coeur, MO 63167, USA
Derived from rice genomic sequences generated from the Monsanto
Rice Genome Sequencing project. Please see
http://www.rice-research.org for more information. The sequence
data were produced primarily in the laboratories of Dr. Leroy Ho
at the University of Washington in Seattle.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa microsatellite MRG6004 containing marker R1479, genomic sequence.

AV032570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 120) Brockmann, B., Schnieders, F., Kunze, B., Krawczak, M. and Schmidtke, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa Oryza sativa Coryza sativa Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 224)
Tao,N., Barbazuk,W.B., Liu,J., Wu,K. and Barry,G
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/db_xref="taxon:10116"
<1. .>120
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80. .120
/note="intronic"
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/db_xref="taxon:4530"
1. .224
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Pred. No. 2.5e+02;
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Primer B:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Substitute of TX Health Science Center, San Antonio Univ. OF TX Health Science Center, San Antonio, TX 78385, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G35045.1 GI:2358168
STS; STS sequence; primer; sequence tagged site.
human vector=pBluescript host=XL1 Blue Alu PCR products
chromosome 3 radiation hybrids cloned into pBs.
                                                                                                                                   Similarity
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PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7703 Floyd Curl Dr., San Antonio, Tel: (210)567-3842
Fax: (210)567-6781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDB_DSEG: D3S4038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 239) Naylor,S.L., Garcia,D.K., Kerbacker,K., O'Connell,P. and Stanton,V. Human Chromosome 3 STS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Susan L. Naylor
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                                                                                                                   Conservative
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Extension:
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                                                                                                                                                                                                          complement(195.
                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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83. .100
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Submitted (24-JUL-1998) to the DDBJ/EMBL/GenBank databases. Takeshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (sites)
Watanabe, T.K., Hishiqaki, H., Kanemoto, N., Miyakita-Mizoguchi, A.,
Oga, K., Okuno, S., Ono, T., Tsuji, A., Hayashi, H., Adachi, M.,
Yamasaki, Y., Iriye, Y., Takahashi, E., Takaqi, T., Nakamura, Y. and
                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                           microsatellite polymorphism; microsatellite repeat; repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMRPTPLM 309 bp DNA linear pr
Human microsatellite dinucleotide repeat polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K Watanabe, Otsuka Pharmaceutical Co., Ltd., Otsuka GEN Researcl Institute; 463-10, Kagasuno, Kawauchi-cho, Tokushima, Tokushima, 771-0192, Japan (E-mail:watanabe@otsuka.genome.ad.jp, Tel:81-886-65-2888, Fax:81-886-37-1035)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus, OTSUKA clone, sequence, sequence tagged site. AU026129
                                                                                                                                                                                                                                               Sainz
                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus DNA, clone:OT58.09/882h07. Rattus norvegicus
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STS.
                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                       Homo sapiens (tissue library: Bluescript) DNA
                                                                                                                                                                                                                                                                                                                                                               polymorphism.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/clone="0T58.09/882h07"
/note="0T58.09/882h07P=5'.-CGATCCTATCTCCGTGTCCTC-3',
OT58.09/882h07R=5'.-GTCATTCTCTAACTTCCACAGGTG-3'"
a 42 c 71 g 126 t
                                                                                       /tissue_lib="Bluescript"
212. .248
                                                                                                                                                                                                                                           and Pulst, S.-M.
             /note="polymorphism"
/rpt_family="microsatellite"
/rpt_type=tandem
82 c 52 g 62 t
                                                                                                                           /map="22q12"
                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                       Location/Qualifiers
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Pred. No. 2.3e+02;
); Mismatches 0;
           52 g
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DEFINITION Human STS UT1400, sequence tagged site.
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                                                                                                   41 AGAAACAAACAAACAAA 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STS; PCR primer; microsatellite marker; microsatellite repeat; repeat polymorphism; sequence tagged site; tetranucleotide rep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence tagged sites from the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human chromosome 10 STS UT925, sequence tagged site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Annealing: 60C 10sec Extension: 72C 20sec
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Primer B: GTCCTTGTGAGAAACTGGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L16357.1 GI:308719
                  HUMUT1400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e-mail: sts@corona.med.utah.edu
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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a 82 c 94 g
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                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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                                                                                                                                                                                        100.0%; Score 21; DB 11; 100.0%; Pred. No. 2.2e+02;
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100.0%; Pred. No. 2.3e+02;
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                   407 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STS; PCR primer; STS sequence; microsatellite marker; microsatellite repeat; repeat polymorphism; sequence tagged site.
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2160 Eccles Institute of Human Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted by: Utah Center for Human Genome Research University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence tagged sites from the human genome Unpublished (1993)
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                                                                                                                                                                                                                                                                                                                                             polymorphism.
L12265
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Extension: 72C 20sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32P-label: B Primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer A: GATGGGAGGACTGCTTAAGC
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                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (D8S320 locus) DNA sequence, tetranucleotide repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mg++: 1mM
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                                                                    Tetranucleotide repeat polymorphism at the D8S320 locus Hum. Mol. Genet. 2, 1512-1512 (1993)
                                                                                                                          and Ward, K
                                                                                                                                              Riley,R., Nelson,L., Lu,J., Robertson,M., Ballard,L.L., Connolly,J.
                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                          tetranucleotide repeat polymorphism.
                                                                                                                                                                                                                                                                                                                      L12265.1 GI:388013
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                                                                                                                                                                     (bases 1 to 497)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                      sapiens DNA.
                                             Location/Qualifiers
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/organism="Homo sapiens"
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                                                        Local Similarity
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1 agaaacaaacaaacaaacaaa 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted by: Utah Center for Human Genome Research University of Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: sts@corona.med.utah.edu
Primer A: GCATATACCTGGCAATGGCAAAAAC
Primer B: GTCAATTTCCAGAGACTGTAAAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gerken,S.C., Matsunami,N., Lawrence,E., Carlson,M., Moore,M., Ballard,L., Melis,R., Robertson,M., Bradley,P., Elsner,T., Tingey,A., Rodriguez,P., Albertsen,H., Lalouel,J.-M. and White,R. Genetic and physical mapping of simple sequence repeat containing sequence tagged sites from the human genome
Unpublished (1993)
                                                                                                                                                                                                                                                                                                                                                                                                  Annealing: 60C 10sec
Extension: 72C 20sec
                                                                                                                                                                                                                                                                                                                                                  Alleles:
                                                                                                                                                                                                                                                                                                                                                                                      Mg++: 2mM
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1 (bases 1 to 497)
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                                      Conservative
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                                                                                                                                               complement(425. .449)
45 c 105 g
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/clone_lib="flow-sorted chromosome 8 specific cosmid
library (LA08NCO1)"
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                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
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/rpt_unit=AAAG
45 c 105 g 62 t
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                            100.0%; Score 21; DB 11; Length 497; 100.0%; Pred. No. 2.2e+02; ative 0; Mismatches 0; Indels (
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181 AGAAACAAACAAACAAA 161
                                                                            Local Similarity
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                            1 agaaacaaacaaacaaa 21
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                                                                                                                                                                                                                                                                                          Derived from dbEST (genbank accession H92026).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Thomas Hudson Whitehead Institute/MIT Center for Genome Research Whitehead Institute for Biomedical Research Whitehead Institute for Biomedical Research 9 Cambridge Center, Cambridge MA 02142 USA
                                                                                                                                                                                                                                                                                                                                                                                             Buffer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protocol
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STS; STS sequence; primer; sequence tagged site.
human STSs derived from sequences in dbEST and the Unigene
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Fax: 617 252 1902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: thudson@genome.wi.mit.edu
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Primer: each 5 ph
dNTPs: each 4 nM
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KCl: 50 mM
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                                                           Conservative
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Annealing: 56 degrees
Polymerization:
PCR Cycles: 35
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1. .21
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97 c 118
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/db_xref="taxon:9606"
/map="183.2 cR from top of Chr7 linkage group"
                                                                                                                                                                                                                                                                              location/Qualifiers
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Pred. No. 2.2e+02;
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primer_bind
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BASE COUNT 15
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G42246/c
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Best Local
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G42246.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Paavola,P., Avela,K., Horelli-Kuitunen,N., Barlund,M.,
Kallioniemi,A., Idaenheimo,N., Kyttaelae,M., de la Chapelle,A.,
Palotte,A., Lehesjoki,A.-E. and Peltonen,L.
High-resolution physical and genetic mapping of the critical region
for Meckel syndrome and Mulibrey Nanism on chromosome 17q22-q23
Genome Res. 9 (3), 267-276 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G42246
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University of Helsinki
Helsinki, Finland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 552)
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STS size: 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Res.
99177349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Kristiina.Avela@Helsinki.fi
                             Gerken,S.C., Matsunami,N., Plaetke,R., Albertsen,H., Ballard,L., Melis,R., Lawrence,E., Moore,M., Holik,P.R., Carlson,M., Zhao,X., Robertson,M., Bradley,P., Elsner,T., Tingey,A., Lalouel,J.-M. and
                                                                                                                                                                              STS; PCR primer; STS sequence; microsatellite DNA; microsatellite marker; sequence tagged site; tetranucleotide repeat.
                                                                                                                                                                                                                                                   Human STS UT6478, sequence
                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                  L30582
                                                                                                                                                                                                                                                                      HUMUT 6478
Genetic and physical mapping of simple sequence repeat containing
                  White, R.
                                                                                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                           Eukaryota; Metazoa; Chordata;
                                                                                                                                                               Homo sapiens DNA.
                                                                                                                                                                                                                 L30582.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(196. .217)
1 107 c 127 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pCYPAC-1; V-type: P1-derived vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Human PAC clone"
/lab_host="E. coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                   GI:604976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATTGTCCAGATTGGTCAGTGG
CCCTCATTTATCTGACAAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 21;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                      561 bp
                                                                                                                                                                                                                                                   61 bp DNA tagged site.
                                                                                                                           Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11;
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JOURNAL COMMENT
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AF254660/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                          REFERENCE
AUTHORS
ORIGIN
                                                                                                                                                                                                                                                                                          REFERENCE
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             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                        VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                             JOURNAL
                                                                                                                                                                              TITLE
                                                                                                                                                                                                                            JOURNAI
                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                           AUTHORS
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                                                               repeat_region
                                                                                                           source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 100.0%; Score 21; DB 11; Local Similarity 100.0%; Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l agaaacaaacaaacaaacaaa 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence tagged sites from the human genome
Unpublished (1994)
Submitted by: Utah Center for Human Genome Research University of
Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cycles
C 10 s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C 10 sec. 64 C 10 sec. 72 C 20 sec. Mg++: 1.00 r 60 C 10 sec. 72 C 20 sec. Mg++: 1.00 r Gel: Acrylamide 7%, Formamide 32%, Urea 34%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e-mail: sts@corona.med.utah.edu
primer A: TACACTCCAGCCTGGGCAAC
Primer B: CTCCTCAGCAGTCTCCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alleles:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              End to Label: Primer B
                                                                                                                                                                                                                                                                                                                                                                                                        Tetrao urogallus microsatellite AF254660
                                                                                                                                       Segelbacher,G.
Direct Submission
Direct Submission
Submitted (12-APR-2000) Unit of Wildlife Research and Management,
TU Munich, Am Hochanger 13, Freising 85354, Germany
                                                                                                                                                                                                                                                         Segelbacher,G., Paxton,R. and Steinbrueck,G. Characterization of hypervariable microsatellites in Capercaillie
                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Tetraonidae; Tetrao. 1 (bases 1 to 617)
                                                                                                                                                                                                                                                                                                                                       Tetrao urogallus
                                                                                                                                                                                                                                                                                                                                                                                          AF254660.1 GI:13926063
                                                                                                                                                                                                                                                                                                                                                                                                                                          AF254660
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                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                        western capercaillie.
                                                                                                                                                                                                                                            (Tetrao urogallus)
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167. .343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /standard_name="STS UT6478"
167. .186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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1. .617
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               /rpt_type=tandem
156 c 69
                                                                                                                            Location/Qualifiers
                                              /note="microsatellite TUT8"
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64 C 10 sec. 72 C 20 sec.
9ec. 72 C 20 sec. Mg++: 1.00
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                 69 g
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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BG
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seq length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  654821
                                                                                                                                                                                                                                                                                                                                                                                        Match Length
                                                                                                                                                                                                                                                                                                                                                                                                    Query
    US-09-899-718A-2
29
1 cacgcaaaggcgcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cacgcaaaggcgcgtcggccagccacgac
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4 US-09-103-840A-1
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Result

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53.8	53.8	54.5	54.5	54.5	54.5	54.5	54.5	54.5	55.2	55.2	55.2	55.2	55.2	55.2	55.2	55.9	55.9
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us-09-060-756-187	US-08-884-866A-21	US-08-630-915A-17	US-08-751-512-7	US-08-690-096-11	US-07-940-605A-11	US-08-998-416-150	US-09-194-905-4	US-08-671-892A-8	US-09-370-700-1	US-09-036-987A-1	US-09-105-537-32	US-09-041-886-18	US-09-043-303-5	US-08-913-362-29	US-09-043-303-3	US-09-103-840A-1	US-08-724-394A-22
187,	Sequence 21, Appl	Sequence 17, Appl	Sequence 7, Appli	11,	Sequence 11, Appl	15	4	Sequence 8, Appli	Sequence 1, Appli	1, A	Sequence 32, Appl	Sequence 18, Appl	Sequence 5, Appli	Sequence 29, Appl	Sequence 3, Appli	Sequence 1, Appl	Sequence 22, Appl

ALIGNMENTS

RESULT 1 US-08-162-809-9

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; NAME/KEY:
; LOCATION:
US-08-162-809-9
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; Patent No. 5457048
Query Match
Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                   TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Fereydoun G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
NUMBER OF SEQUENCES: 26
                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
STREET: 43
CITY: San
                                                                                                                                                                                 TYPE: nucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                     LENGTH: 3546 base pairs
 l Similarity
21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           San Diego
: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: CAMPBELL AND FLORES 4370 La Jolla Village Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        United States of America
 Conservative
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2..2920
                                                                                                                                                                linear
                 64.1%;
Score 18.6; D
Pred. No. 18;
0; Mismatches
 0;
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Sequence Sequence

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; NAME/KEY:
; LOCATION:
US-08-162-809-13
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Best Local Similarity 84.0
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                                                                                                                                                                                 Sequence 1, Application US/09095443 Patent No. 6342593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PTELECOMMUNICATION INFORMATION: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Fereydoun G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS (
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                         TITLE OF INVENTION: DIAGNOSIS AND TREATMENT TITLE OF INVENTION: OF ALP RELATED DISORDERS NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                              2408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                               APPLICANT: Plowman, Gr
APPLICANT: Peles, Eior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid STRANDEDNESS: both TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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                                                                                                                                                                                                                                                                                                               3 cgcaaaggcgcgtcggccagccacg 27
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                                                                                                                                                                                                                                                                                              CGCAAATTCACGTCGGCCAGCGACG 2432
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4370 La Jolla Village Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3591 base pairs
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                                                                                                                                              Plowman, Gregory
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                                                                                                                                                                                                                                                                                                                                                                                  64.18;
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Pred. No. 18;
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US-09-095-443-1
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US-09-103-840A-2
                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: FLEISCHMAN, Robert D.

APPLICANT: WHITE, OWEN R.

APPLICANT: FRASER, Claire M.

APPLICANT: VENTER, John C.

TITLE OF INVENTION: DAN SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

TITLE OF INVENTION: TUBERCULOSIS

FILE REFERENCE: 24366-20007.00

CURRENT APPLICATION UNMBER: US/09/103,840A

CURRENT FILING DATE: 1998-06-24
                                                                                                                                                           NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                          sequence 2, Application US/09103840A
Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
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                                                                                   TYPE: DNA ORGANISM: Mycobacterium tuberculosis
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COUNTRY: U.S...
"TD: 90071-2066
"FADABLE F
                OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FastSEQ for Windows 2.0 CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAN: (213) 955-0440
TELEPAN: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/0 FILING DATE: June 12, 19 ATTORNEY/AGENT INFORMATION: NAME: Warburg, Richard J
                                                                                                                                      LENGTH: 4403765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1846 GCCATGGCGGTTCGGCCAGCCACCAC 1871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327 REFERENCE/DOCKET NUMBER: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US FILING DATE: Herewith
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80.8%;
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31;
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Query Match Best Local Similarity

60.0%; 75.9%;

Score 17.4; Pred. No. 38;

DB 4;; ; s 7;

Length 4403765;

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Gaps

0;

Matches

22;

Conservative

0;

Mismatches

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; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: WHITE, OWED R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, JOHN C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                   TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9503
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Fereydoun
TITLE OF INVENTION: NOVEL EPH-
TITLE OF INVENTION: NUCLEOTIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                     TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                         APPLICATION NUMBER:
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mes 21; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                San Diego
CHARACTERISTICS:
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: United States
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4370 La Jolla Village Drive, Suite 700
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                                                       (619)
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77.8%;
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NOVEL EPH-RELATED TYROSINE KINASES.
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                                                                                                                                                                                                       US/08/162,809
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Pred. No. 38;
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US-08-162-809-3
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                                                       Matches
                                                                 Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NERAL INFORMATION: Elena b.
APPLICANT: Sajjadi, Fereydoun G.
APPLICANT: Sajjadi, Fereydoun G.
APPLICANT: SAJJADI, FORMATION: NOVEL EPH-RELATED TYROSINE KINASES,
1613 CGCAAATTCACGTCGGCCAGCGATG 1637
                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                    NAME/KEY:
LOCATION:
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LOCATION:
                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Diego
STATE: California
CCOUNTRY: United States of America
                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                             TELEPHONE:
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TOPOLOGY: linear
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                cgcaaaggcgcgtcggccagccacg 27
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DEDNESS: both
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4370 La Jolla Village
                                                     Conservative
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2..2167
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                                                                 Score 17;
Pred. No.
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Pred. No. 81;
                                                     Mismatches
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                                                                              Length 3059;
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US-08-162-809-19
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                                                                                                                                                                                                                                                         sequence 1, Application US/08460806 Patent No. 5747241
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                            GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Fereydoun G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                1679 CGCAAATTCACGTCGGCCAGCGATG 1703
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                       TITLE OF INVENTION:
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                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
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                              CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 58.6%;
Local Similarity 80.0%;
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                                                                  STREET:
                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
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                  COUNTRY:
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                                                                 1755 S. Jefferson Davis Highway, Suite 400
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HONDA, YOSHIKAZU
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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SAITO, IZUMU
                U.S.A.
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                                                                                                 OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT
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Best Local Similarity
Matches 21; Conserv
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
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APPLICATION NUMBER: US/C
FILING DATE: 19-0CT-1994
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
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                                                                                                                                                                                                                                                                                        APPLICANT: MIYAMURA, TATSUO APPLICANT: SAITO, IZUMU
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                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                            TITLE OF INVENTION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                      CITY: Arlington STATE: Virginia
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                                                                                                                                                        E: P.C.
1755 S. Jefferson Davis Highway, Suite 400
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                                                                                                                                                                                                                                      HONDA, YOSHIKAZU
VENTION: DIAGNOSTIC REAGENT FOR HEPATITIS C
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                                                                                                      U.S.A.
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   PatentIn Release #1.0, Version #1.25
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Pred. No. 96;
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Gaps

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CURRENT APPLICATION DATA:

US/08/325,630

APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435

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Db 11075 GGCGCGTCGGCGAGCCGCGA 11056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-325-630-1
                                                                                                                                                                                                  SOFTWARE: FastSI
SEQ ID NO 30
LENGTH: 13842
TYPE: DNA
                                                           Query Match
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 30, Applicat Patent No. 6265202 GENERAL INFORMATION:
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TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 base pairs
TYPE: nucleic acid
STRANDENNESS: double
                                                                                                                                                                                                                                                  APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Wae, V.
APPLICANT: APPLICANT: APPLICANT: APPLICANT: Liao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PastSEQ for Windows Version 3.0
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CLONE: J1-1325
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NAME: Oblon, No. 5750331man F.
REGISTRATION NUMBER: 24,618
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APPLICATION NUMBER: US 07/956,993
FILING DATE: 06-OCT-1992
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LOCATION:
                     9 ggcgcgtcggccagccacga 28
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09105537A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                    57.9%;
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75.0%;
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                                                                                      Score 16.8; DB 4; Length 13842; Pred. No. 1e+02;
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Pred. No. 96;
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                                                                       Mismatches
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APPLICANT: ASHLEY, GATY
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, MARY C.
APPLICANT: MCDANIEL, ROBERT
APPLICANT: TANG, Li
                                                                                                                                                                                           US-09-320-878-19
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; ORGANISM: Streptomyces venezuelae
US-09-105-537-5
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                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 38506
TYPE: DNA
ORGANISM: Streptomyces venezuelae
                                                                                   Matches
                                                                                                                      Query Match
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Patent No. 6117659
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SEQ ID NO 5
LENGTH: 36778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 90.0 Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: 60/100,880
EARLIER FILING DATE: 1998-09-22
EARLIER APPLICATION NUMBER: 60/087,080
EARLIER FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: CIP OF 09/073,538
EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER FILING DATE: 1997-04-30
EARLIER APPLICATION NUMBER: 60/119,139
EARLIER FILING DATE: 1999-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE FILE REFERENCE: 300622002120
CURRENT APPLICATION NUMBER: US/09/320,878A
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: CIP OF 09/141,908
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/105,537A CURRENT FILING DATE: 1998-06-26 NUMBER OF SEQ ID NOS: 43
10958 GGCGCGTCGGCGAGCCGCGA 10939
                                                                                                     Local Similarity
                 9 ggcgcgtcggccagccacga 28
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                                                                                 Conservative
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90.0%;
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Pred. No. 1
                                                                               Mismatches
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                                                                                                                      DB 3;
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US-08-913-362-3
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Patent No. 6287574
GENERAL INFORMATION:
                                                                 Best
                                                   Matches
                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO ORIGINAL SOURCE:
ORIGINAL SOURCE:
OPPANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29.7
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC computable
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
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LENGTH: 710 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                 FEATURE:
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                                                Match 56.6%; Local Similarity 76.9%; nes 20; Conservative
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173..643
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116..172
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                                                                   Score 16.4; DB 4;
Pred. No. 1.4e+02;
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             Query Match
Best Local :
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APPLICANT:
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TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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LENGTH: 830 base pairs
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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TELLEFAX: 904136
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 Similarity 20; Conserv
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Rioux, Clement
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(202)672-5399
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Conservative
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SYSTEM: PC-DOS/MS-DOS
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200..667
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                56.6%;
76.9%;
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              Score 16.4; DB 4; Length 830; Pred. No. 1.4e+02;
  Mismatches
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Db 387 GCATCGGCGCTCCGCCATTTACGAC 412

Search completed: July 31, 2002, 12:20:34 Job time: 11657 sec

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Result		e Onerv			COMMENTED	
No.	Score		Length	BB	ID	Description
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	19.8	68.3	255	9	AA227176	AA227176
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	19.8	68.3	984	10	BG024310	BG024310 60227447
	19.8	68.3	2306	11	BC004149	BC004149
თ	19.4	66.9	1028	10	BE733309	BE733309
7	19.4	66.9	1100	10	BE893877	BE893877
8	19.4	66.9	1829	12	AQ782504	AQ782504
و	19.2	66.2	325	10	D48137	D48137 RICS14202A
10	19.2	66.2	1096	12	CNS04XLD	AL311818 Tetraodon
	19	65.5	290	9	AW972385	AW972385
	19	65.5	326	9	AV433974	AV433974
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	19	65.5	452	o	AV430263	AV430263 AV430263
	19	65.5	479	9	BB855054	
c 16	19	65.5	509	9	AV435479	AV435479
c 17	19	65.5	517	0	****	COCCUTE COCCUTE

ALIGNMENTS

	FEATURES Source	REFERENCE AUTHORS TITLE JOURNAL COMMENT	RESULT 1 N46230/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM
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BASE COUNT
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cDNA clone IMAGE:664000 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                White,Y., Wylie,T., Waterst
WashU-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                          Insert Length: 1138 Std Error: 0.00 Seq primer: -28ml3 revl ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA227176.1 GI:1848846
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                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 247.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 286 1800
314 286 1810
       44 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lesions from one patient was kindly provided by Dr. Kevin G. Becker (NINDS/NIH). "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pT7T3D (Pharmacia) with a modified polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5']
/clone_lib="Stratagene NT2 neuronal precursor 937230"
/tissue_type="neuroepithelial cells"
/dev_stage="Ntera-2 neuroepithelial cells"
                                                                                                                      /note="Organ: brain; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer
                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="GDB:5425859"
                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
                                                                                                                                                                    /lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                    /clone="IMAGE:664000"
                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.3%; Score 19.8; DB 1U;
91.3%; Pred. No. 4.5e+02;
Nismatches 2;
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COMMENT

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4 gcaaaggcgcgtcggccagccac 26

Matches

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Conservative

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AUTHORS

SOURCE KEYWORDS VERSION ACCESSION

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 GCAAAGGCGCGTCGGCCGGGCAC 75
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    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMAGE: 358780 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        zel2e03.rl Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 321.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                          65
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                                                                                                        NbHL19W."
a 107 c
                                                                                                                                                                                                       double-stranded cDNA was size selected, ligated to Ecc RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Ecc RI sites of a modified pT7T3 vector (Pharmacia). Library went through accounts.
                                                                                                                                                                  (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the
                                                                                                                                               same fetus as the fetal lung library, Soares fetal lung
                                                                                                                                                                                                                                                                                            /lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:358780"
                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="19 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Soares_fetal_heart_NbHH19W"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="GDB:1275324"
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  Score 19.8; DB 10; Length 350; Pred. No. 5.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   4 gcaaaggcgcgtcggccagccac 26
Submitted (01-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 2306)
                                                                                                                                                                                                                                                          Homo sapiens, clone IMAGE:2819393, mRNA
BC004149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue Procurement: Louis Staudt, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
                                                                      Direct Submission
                                                                                          Strausberg, R
                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                        BC004149.1 GI:14708750
                                                                                                                                                                                                                                                                                                      BC004149
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Plate: LLAM10006 row: n column: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BG024310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph, Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 356 c 249 g 187 t
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                                                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov plate: LLCM540 row: k column: 23
High quality sequence stop: 136.
                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1028)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
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contact: amadanésystemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
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Tissue Procurement: DCTD/DTP
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/db_xref="taxon:960b"
/clone="IMAGE:2819393"
/tissue_type="Lung, small cell carcinoma"
/clone_lib="NII_MGC_7"
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                                               /organism="Homo sapiens"
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/clone_lib="NIH_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
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/db_xref="taxon:9606"
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955 CACCCAAAGGAGGCCGCCCAACCACGAC 983
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Tissue Procurement: ATCC/DCTD/DTP
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Plate: LLAM9754 row: c column: 11
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Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GCCACCAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." a 351 c 296 g 51 t
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                                                                                                                                                                                                                                                                                    /tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skir, Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo_
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/db_xref="taxon:9606"
/clone="IMAGE:3921346"
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AQ782504

HS 3174_A2_G10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3174 Col=20 Row=M, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu plate: 3174 row: M column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS
                                                                                                                                                    Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                   D48137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 1829.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1829)
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              Unpublished (1995)
Contact: Takuji Sasaki
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                                                    Sasaki,T., Miyao,A. and Yamamoto,K. Rice cDNA from callus 1995
                                                                                                                                                                                                                                  D48137.1
                                                                                                                                                                                                                                                                     RICS14202A Rice green shoot Oryza sativa cDNA, mRNA sequence
                                                                                                                                                                                                                                                                                         D48137
                                                                                                                                                                                          Oryza sativa.
National Institute of Agrobiological Resources
                                                                                                                Ehrhartoideae;
                                                                                                                                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                  (bases 1 to 325)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (206) 616-3887
; jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
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                                                                                                                  Oryzeae; Oryza.

 Mismatches

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AUTHORS
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Best Local S
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                                                                                                                                                                                                Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                               Bernot,A. and Weissenbacn,J.
Characterization and repeat analysis of the compact genome of the freshwater pufferfish tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 1096)
Crollius,H.R., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL311818.1 GI:9544686
GSS; genome survey sequence.
Tetraodon nigroviridis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

1 (bases 1 to 1096)
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305-8602,
                                                                                                                                                                                       genome. For more information, please t
http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 66.2%;
Similarity 80.8%;
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                    241 a
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Location/Qualifiers
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    /clone_lib="A"
/note="Genoscope sequence ID : COAA053BC08A1-end :
/note="Genoscope sequence ID : COAA053BC08A1-end :
                                                                        /db_xref="taxon:99883"
/clone="053E16"
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/note="Green shoot (8 days old)"
115 c 73 g 49 t
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/db_xref="taxon:4530"
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                                                                                                                                                                                                  AV433974 Porphyra yezoensis TU-1 Porphyra yezoensis PM036f02_r 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                 22;
       gametophyte of a marine
                     Generation of 10,154 expressed sequence tags from a leafy
                                                 1 (bases 1 to 326)
Nikaldo, I., Asamizu, E., Nakajima, M., Nakamura, Y., Saga, N. and
                                        Tabata, S
                                                                                                                         Porphyra yezoensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                        Porphyra.
                                                                                                    Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae;
                                                                                                                                      Porphyra yezoensis.
                                                                                                                                                                           AV433974.1 GI:8589199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: johng@tigr.org
Plate: 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 301 838 3528 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assessment of gene expression patterns in a model of metastasis using a 19,200 element cDNA microarray Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quackenbush,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="Vector: pBluescriptSKm"
/6 c 81 g 66 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                               65.5%;
81.5%;
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87.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                             Score 19;
Pred. No.
red alga, Porphyra yezoensis
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                                                                                                                                                                                                                                                                                                                                                                                                                             DB 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length 290;
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FEATURES
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                                                                                                                                                                            BASE COUNT
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                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                             source
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276 CGCACAGGCGCGACGGCGACGAC 250
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                                   w
                                                                                      Local Similarity
                                 cgcaaaggcgcgtcggccagccacgac 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The First Laboratory for Plant Gene Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Generation of 10,154 expressed sequence tags from a leafy gametophyte of a marine red alga, Porphyra yezoensis DNA Res. 7, 223-227 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \Lambda V4\,35705 Porphyra yezoensis TU-1 Porphyra yezoensis cDNA clone p_{M0.61} c_{0.4} - r 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Porphyra yezoensis
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Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 416)
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1: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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                                                                                                                                                                                  47 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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/clone="PM036f02_r"
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                                                                                                                                                                                                                                                                                       /organism="Porphyra yezoensis"
/strain="TU-1"
                                                                                                                                                                                                                                     /clone="PM061c04_r"
/clone_lib="Porphyra yezoensis TU-1"
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81.5%;
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Pred. No. le+03;

 Mismatches

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                                                                                                            Score 19;
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                     JOURNAL
                                                                  TITLE
                                                                                                                                                                                                                                                   AUTHORS
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AV430263 Porphyra yezoensis TU-1 Porphyra yezoensis cDNA clone PL015h12_r 5', mRNA sequence.
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Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Generation of 10,154 expressed sequence tags from a leafy
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                                                                           Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Shii,
,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
,Y., Ito,M., Kishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.,
,Sakani,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
,Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
,Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa
,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T.,
,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T.,
,Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.,

RIKEN PROVENCIANASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gametophyte of a marine red alga, Porphyra yezoensis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Erika Asamizu
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                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                            BB855054.1 GI:17096508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BB855054
Contact: Yoshihide Hayashizaki
                     Unpublished (2001)
                                                               RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                    nouse mouse.
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/clone="pL015h12_r"
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Pred. No. 1.1e+03;
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          further details
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 81-45-503-9222 Fax: 81-45-503-9216
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Database

Minimum DB Maximum DB

Scoring table:

Perfect score:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. // SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA199.DAT: *
// SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA2001.DAT: *

SUMMARIES

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62.1	62.8	63.4	63.4	64.1	64.1	64.1	67.6	67.6	Query Match Length DB
3810	2557	3641	1511	3591	3546	991	2474	2473	Length
21	23	22	22	16	16	21	22	22	DB
AAC77273	ABL18098	AAF74767	AAF74776	AAQ90658	AAQ90656	AAF14887	AAL05201	AAL05200	ID
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Mycobacterium tube

RESULT 1
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ID AAL052 21-NOV-2001 (first entry) AAL05200; AAL05200 standard; DNA; 2473

Human reproductive system related antigen DNA SEQ ID NO: 7888.

Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ${\tt ds.}$

Homo sapiens.

WO200155320-A2

02-AUG-2001.

17-JAN-2001; 2001WO-US01339 2000US-0179065. 2000US-0180628. 2000US-0184664.

31 JAN-2000; 04-FEB-2000; 24-FEB-2000; 02-MAR-2000; 16-MAR-2000; 17-MAR-2000; 19-MAY-2000; 19-MAY-2000; 2000US-0186350 2000US-0189874 2000US-0190076 2000US-0198123 2000US-0205515 2000US-0204867 2000US-0214886 2000US-0214885

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17-NO
                                                                                                The present invention provides the protein and coding sequences o number of human reproductive system related antigens. These can be in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoprotein of the invention.
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8-APR-2000;
9-MAY-2000;
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3-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
  06-SEP-2000
08-SEP-2000
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29-SEP-2000
20-CCT-2000
21-CCT-2000
21-CCT
2000US-0241808
2000US-0241809
2000US-0244617
2000US-0246474
2000US-0246475
2000US-0246476
2000US-0246476
2000US-0246523
2000US-0246524
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2000US-0246610
2000US-0246610
2000US-0246611
2000US-0249216
2000US-0249211
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2000US-0233064
2000US-0233065
2000US-0234223
2000US-0234224
2000US-0234998
2000US-0235484
2000US-0235484
2000US-0235834
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2000US-0239935.
2000US-0239937.
2000US-024960.
2000US-0241781.
2000US-0241785.
2000US-0241786.
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2000US-0231414
2000US-0231414
2000US-0232080
2000US-0232081
2000US-0232981
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AAF14887/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
                                                                                                                                                                                          Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              including cancer. The pre protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a
                                                                                                                                                   Trichoderma
                                                                                                                                                                                                                                                                                                                                                     Trichoderma
                                                                                                                                                                                                                                                                                                                                                                                                       13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF14887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF14887 standard; cDNA; 991 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1679 CACGCAAAGGCCCGTCAGCTTGCCAC 1654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2474 BP; 431 A; 863 C; 812 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rsolated nucleic acid molecule encoding a reproductive system antigen
is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen
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22-MAR-2000; 2000WO-US07781.
                                                                                                 WO200056762-A2
                                            28-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 cacgcaaaggcgcgtcggccagccac 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0250391.
2000US-0251030.
2000US-0251988.
2000US-0256719.
2000US-0251479.
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2000US-0249245

2000US-0249264

2000US-0249265

2000US-0249297

2000US-0249299

2000US-0249300

2000US-0249300
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2000US-0251868.
2000US-0251869.
2000US-0251989.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 7889; 1297pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                        reesei EST
                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.6%;
84.6%;
                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO:7410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 19.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2474;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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W09515375-A

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PN FFT XXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        discovered, possible functions of unknown open reading frames can be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or candom cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF11247 represents ESTs from Aspergillus or iger; AAF11854 to AAF114878 represents ESTs from Aspergillus or iger; AAF11874 to AAF114878 represents ESTs from Aspergillus conject; AAF11874 to AAF11875 represents ESTs from Trichoderma reesei, which are call specifically claimed in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 89; Page 2992; 3161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monitoring differential expression of genuses fluorescence-labeled nucleic acids substrate of expressed sequence tags -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NOVO ) NOVO NORDISK BIOTECH INC (NOVO ) NOVO NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berka RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      same genes in one or more second filamentous fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 991 BP;
                                                                                                       Gallus sp
                                                                                                                                           prognosis;
                                                                                                                                                                                             Eph-related
                                                                                                                                                                                                                                   11-NOV-1995
                                                                                                                                                                                                                                                                     AAQ90656;
                                                                                                                                                                                                                                                                                                         AAQ90656 standard;
                                                                                                                                                                                                                                                                                                                                                                                               621 CACGCAAAGGCACGTCCCCCAGTCA 597
                                                                                                                                                                                                                                                                                                                                                                                                                               1 cacgcaaaggcgcgtcggccagcca
                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rey MW,
                                                                                                                                                                                                 PTK Cek10 cDNA
                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                 (first entry)
                                                  Location/Qualifiers 2..2923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 A; 290 C; 269 G;
                                                                                                                                                                                                                                                                                                         cDNA; 3546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shuster JR,
                                                                                                                                                              tyrosine-kinase; PTK; cancer; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.1%;
84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18.6;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DВ
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cells and a
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RESULT
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       P-PSDB; AAR75710
                                   Pasquale
                                                                      03-DEC-1993;
                                                                                        07-SEP-1994;
                                                                                                         08-JUN-1995.
                                                                                                                          WO9515375-A.
                                                                                                                                                                                 Gallus
                                                                                                                                                                                                 prognosis;
                                                                                                                                                                                                        Cek10+; Eph; protein
                                                                                                                                                                                                                            Eph-related
                                                                                                                                                                                                                                              11-NOV-1995
                                                                                                                                                                                                                                                                                  AAQ90658
                                                                                                                                                                                                                                                                                                                            2363 cgcaaattcacgtcggccagcgacg 2387
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3546 BP;
                                                   (LJOL-) LA JOLLA CANCER RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eph-related protein tyrosine kinase(s) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPT; 1995-215256/28.
P-PSDB; AAR75708.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                      3 cgcaaaggcgcgtcggccagccacg
                                                                                                                                                                                                                                                                                                   տ
                  1995-215256/28
                                                                                                                                                                                sp.
                                   EB,
                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 63-67; 129pp; English.
                                                                                                                                                                                                  SS
                                                                                                                                                                                                                           PTK Cek10+ cDNA
                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                             (first entry)
                                  Sajjadi
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                                                                     93US-0162809
                                                                                      94WO-US10140
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                                                                                                                                                    Location/Qualifiers 2..2968
                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                             742
                                                                                                                                                                                                                                                                                 cDNA; 3591
                                                                                                                                                                                                                                                                                                                                                                         64.18;
84.08;
                                                                                                                                                                                                        tyrosine-kinase; PTK; cancer; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                            A; 1100 C; 1031 G;
                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOUND
                                                                                                                                                                                                                                                                                                                                                                         Score 18.6;
Pred. No. 1
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Matches
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      The present invention describes a basic helix loop helix (bHLH) type transcription factor designated DEC2. DEC2 can be used as a tool in the development of drugs for the treatment and prevention of disorders involving cell differentiation and proliferation. The present sequence encodes the specifically claimed human DEC2b protein, as given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2408
                                                                                      Claim 1; Page 63-68; 83pp; Japanese.
                                                                                                                       DEC2 is a basic helix loop helix protein of the DEC family for use in development of drugs for treatment of disorders of cell differentiation and proliferation
                                                                                                                                                                                                           Fujimoto K,
                                                                                                                                                                                                                                                                19-AUG-1999;
                                                                                                                                                                                                                                                                                         19-JUN-2000;
                                                                                                                                                                                                                                                                                                                     01-MAR-2001.
                                                                                                                                                                                                                                                                                                                                              WO200114551-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEC2a; DEC2b; bHLH type transcription factor; DEC2; DEC1; basic helix loop helix protein; cell differentiation; pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human DEC2b encoding cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF74776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3591 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               originate from the same gene by alternative splicing. Cek10 expression was prominent in the kidney, and to a lesser extent in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid insertion in the juxtamembrane domain, were isolated from chick embryo library in lambda gtll. Cekl0 and Cekl0+ may originate from the same gene by alternative splicing. Cekl0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel EPH-related PTK cDNA clone Cekl0 (given in AAQ90656) and a variant clone, Cekl0+ (AAQ90658), whose product contains a 15-am: \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing
                                                                                                                                                                                                                                      (CHUS ) CHUGAI SEIYAKU KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF74776 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgcaaaggcgcgtcggccagccacg 27
                                                                                                                                                                                    2001-202935/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cgcaaattcacgtcggccagcgacg 2432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 84.0
21; Conservative
                                                                                                                                                                      AAB70693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 78-82; 129pp; English.
                                                                                                                                                                                                           Shin M,
                                                                                                                                                                                                                                                                                         2000WO-JP03991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                99JP-0233286
                                                                                                                                                                                                                                                                                                                                                                /product= "DEC2b"
/note= "bHLH type transcription factor"
                                                                                                                                                                                                                                                                                                                                                                                                              2..1456
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         753 A; 1112 C; 1042 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.1%;
                                                                                                                                                                                                           Kato
                                                                                                                                                                                                                                                                                                                                                                                                Q)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18.6;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO:11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           differentiation; proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        684 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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invention

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                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF74767 standard; cDNA; 3641 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human DEC2a encoding cDNA sequence SEQ ID NO:1.
                                                                                                                           Sequence 3641 BP; 994 A; 922 C; 836 G; 889 T; 0 other;
                                                                                                                                                     present invention.
                                                                                                                                                                     encodes the specifically claimed human DEC2a protein, as given in the
                                                                                                                                                                               transcription factor designated DEC2. DEC2 can be used as a tool in
the development of drugs for the treatment and prevention of disorders
involving cell differentiation and proliferation. The present sequence
                                                                                                                                                                                                                           The present invention describes a basic helix loop helix (bHLH) type
                                                                                                                                                                                                                                                    Claim 1; Page 48-55; 83pp; Japanese.
                                                                                                                                                                                                                                                                                                              DEC2 is a basic helix loop helix protein of the DEC family for use in
                                                                                                                                                                                                                                                                                                                                                                                                           (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                         19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUN-2000; 2000WO-JP03991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200114551-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEC2a; DEC2b; bHLH type transcription factor; DEC2; DEC1; basic helix loop helix protein; cell differentiation; proliferation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                            development of drugs for treatment of disorders of cell differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               769 aggcaaaggcgcgggggggggggcgcgcgtc 796
896 aggcaaaggcgcggggggggggcgcgcgtc 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                        2 acycaaaggcgcgtcggccagccacgac 29
                                                                                                                                                                                                                                                                                                                                                       2001-202935/20.
                                                                    63.4%;
Similarity 78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                 Shin M,
                                                                                                                                                                                                                                                                                                                                                                                                                                          99JP-0233286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "bHLH type transcription factor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "DEC2a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.4%;
78.6%;
                                                       0;
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Pred. No. 1.
                                                                    Score 18.4; DB 22; Length 3641; Pred. No. 1.4e+02;
                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1511;
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                                                         Indels
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RESULT
ABL18098
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RESULT
                                                                                                                  Matches
                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                             capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLI6176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL18098 standard; DNA; 2557 BP.
                                                1779 cccacaggcgcgtcggccatcca 1801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster genomic polynucleotide SEQ ID NO 5767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL18098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pharmaceutical; gene; ds
                                                                                                                                                                                               Sequence 2557 BP; 671 A; 546 C; 563 G; 777 T; 0 other:
                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 5767; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2000; 2000US-191637P
                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                             3 cgcaaaggcgcgtcggccagcca 25
9
                                                                                                                  20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams M,
                                                                                                                  Conservative
                                                                                                                               62.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li PWD,
                                                                                                                  0; Mismatches
                                                                                                                                   Score 18.2; DB 23
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myers EW;
                                                                                                                                                  DB 23; Length 2557;
                                                                                                                   0,
                                                                                                                     Gaps
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vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;

Human ORFX ORF2828 polynucleotide sequence SEQ ID NO:5655.

08-FEB-2001 (first entry)

AAC77273;

AAC77273 standard; cDNA; 3810

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CC immunostimulant; cardiant; thrombolytic; coaquiant; vasotropic; CC antidiabetic; hypotensive; dermatological; immunosuppressive; CC antilnflammatory; antibacterial; antiviral; antifungal; antirheumatic; CC antilnflammatory; antianaemic. The sequences can be used for determining CC the presence of or predisposition to, or preventing or treating CC pathological conditions associated with an ORRY-associated disorder. The CC nucleic acids can be used to express ORRY proteins in gene therapy CC vectors. The proteins and nucleic acids may be used to treat cancers, CC proliferative disorders, neurodegenerative disorders, osteoarthritis, CC graft vs host disease, cardiovascular disease, diabetes mellitus, Pypethension, hypothyroidism, cholesterol ester storage, systemic lupus allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, CC cocturnal haemoglobinuria, antiinflammatory disease; to enhance
                                                                                                                                            Best Local Similarity 80.0
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-1999;
02-APR-1999;
05-APR-1999;
1243 gccatggcggttcggccagccaccac 1268
                                                                                                                                                                                                                                                                                                                       Sequence 3810 BP; 730 A; 1397 C; 1015 G; 664 T; 4 other.
                                                                                                                                                                                                                                                                                                                                                                                            coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypotensive; dermatological; immunosuppressive; antiinflammatory; antiiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; hypothyroidism; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 4829-4832; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acids and peptides derived from open reading frame useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-602362/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAB43064.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thrombosis; contraceptive; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
                          4 gcaaaggcgcgtcggccagccacgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000WO-US08621.
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99US-0127636.
99US-0127728.
                                                                                                                                                                              62.1%;
                                                                                                                                            0,
                                                                                                                                                                              Score 18; I
Pred. No. 2.
                                                                        29
                                                                                                                                            Mismatches
                                                                                                                                                                                                                 DB
                                                                                                                                                                                  .le+02;
                                                                                                                                                                                                                    21;
                                                                                                                                                                                                             Length 3810
                                                                                                                                        0;
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IJ

10-MAR-1999 AAV81748;

(first entry)

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AAV81748
                                     RESULT
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                                                                                                                                                                                                                                                                          CC The invention relates to a novel human tyrosine phosphatase, histidine CC domain-protein tyrosine phosphatase (HB-PTP; AAB29661) and to human CC HB-PTP nucleic acids (AAC81224, AAC8125, AAC81262, AAC81263). The CC HB-PTP pucleic acids (AAC81224, AAC8125, AAC81263). The CC HB-PTP gene is located on chromosome 3p21.3. This region is frequently CC found to be deleted in lung cancers, and is therefore thought to contain CC a tumour suppressor gene. The invention also relates to expression CC vectors and host cells containing human HB-PTP nucleic acids; the CC recombinant production of HB-PTP; anticancer drugs containing HB-PTP; CC gene therapy compositions containing DAA encoding HB-PTP; diagnostic CC reagents containing HB-PTP oligonucleotides; antibodies specific for CC HB-PTP; and an immunoassay method using HB-PTP-specific antibodies for Use in cancer diagnosis and investigation. HB-PTP proteins, nucleic acids and antibodies may be used in the treatment, investigation and diagnosis CC cancers, particularly those of the lung. The present sequence CC represents a human HB-PTP CDNA fragment, CKALI6.
                                                                                                                                                               Query Match
Best Local S
Matches 21
                                                                                          1471
AAV81748 standard; cDNA; 4456 BP
                                                                                                                                                                                                                                                  Sequence 4022 BP; 776 A; 1456 C; 1081 G; 709 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 98-106; 134pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human tyrosine phosphatase with oncostatic activity encoded by a gene frequently deleted in lung cancer, useful for treatment and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-672740/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; histidine domain-protein tyrosine phosphatase; HD-PTP; chromosome 3p21.3; gene deletion; tumour suppressor; cytostatic; lung cancer; tumour; gene therapy; diagnosis; recombinant production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAB29663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anticancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human tyrosine phosphatase HD-PTP cDNA fragment cKAL16, SEQ ID NO:4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-APR-2000; 2000WO-JP02455
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                                                                                                          4 gcaaaggcgcgtcggccagccacgac 29
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                                                                                       gccatggcggttcggccagccaccac 1496
                                                                                                                                                                . Similarity 21; Conserv
                                                                                                                                                               Conservative
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80.8%;
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Pred. No. 2.1e+02
                                                                                                                                                             Mismatches
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                                                                                                                                                                                             Length 4022;
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                AAC81224
                              RESULT 12
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                                                                                                                                 Query Match
Best Local S
Matches 21
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Markby D,
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11-JUN-1997;
11-JUN-1997;
18-JUN-1997;
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type I receptor serine/threonine kinase; cancer; leukaemia; lymphom
neurodegenerative disease; neuronal survival; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human
                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The present sequence encodes human ALP. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, substances that modulate their activity (i.e. agonists and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding specific protein tyrosine phosphatases useful for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-NOV-1998
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                                                                                                                                                                                                                                                                                                                                        including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-1997;
28-APR-1997;
                                                                          1846
                                                                                                                                                                                                          Sequence 4456
                                                                                                                                                                                                                                                proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the
                                                                                                                                                                                                                                                                                           serine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleotides encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2;
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AAC81224
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                                                                                       gcaaaggcgcgtcggccagccacgac 29
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                                                                        gccatggcggttcggccagccaccac 1871
                                                                                                                                 Similarity 80.8
21; Conservative
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 standard; cDNA;
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97US-0044428.
97US-0047222.
97US-0049477.
97US-0049756.
97US-0049914.
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S, Peles E,
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80.8%;
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Pred. No.
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E, Plowman GD;
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The invention relates to a novel human tyrosine phosphatase, histidine CC domain-protein tyrosine phosphatase (HD-PFP; AAB29661) and to human CC HD-PFP pene is located (AAC81224, AAC81225, AAC81262). AAC81263). The CC HD-PFP pene is located on chromosome 3p21.3. This region is frequently CC found to be deleted in lung cancers, and is therefore thought to contain CC a tumour suppressor gene. The invention also relates to expression CC exectors and host cells containing human HD-PFP nucleic acids; the CC recombinant production of HD-PTP; anticancer drugs containing HD-PFP; CC creagents containing HD-PTP, anticancer drugs containing HD-PTP; and an immunoassay method using HD-PTP-specific antibodies specific for CC CC containing HD-PTP oligonucleotides; antibodies specific for CC containing HD-PTP oligonucleotides; antibodies for CC use in cancer diagnosis and investigation. HD-PTP proteins, nucleic acids CC and antibodies may be used in the treatment, investigation and diagnosis CC represents cDNA encoding human HD-PTP.
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Best Local
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                                                                                                                                                                                                                                                                                                      Human tyrosine phosphatase HD-PTP DNA fragment cKAL11, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5234 BP; 1049 A; 1803 C;
                                                                                                                AAC81227
                                                                                                                                                                       AAC81227 standard; DNA; 5436
                                                            23-FEB-2001
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80.8%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local 9
                                                                            Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                            2411 gccatggcggttcggccagccaccac 2436
                                                                                                                                                                                                                                                                                                                                                                              Sequence 5436 BP; 1008 A; 1859 C; 1549 G; 1020 T; 0 other;
                  WO200157182-A2.
                                          Homo sapiens.
                                                                     cytostatic;
                                                                                                        Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21966
                                                                                                                                       06-NOV-2001
                                                                                                                                                                                           AAK67154 standard; DNA; 7016 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human tyrosine phosphatase with oncostatic activity encoded by a gene frequently deleted in lung cancer, useful for treatment and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-672740/65.
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                                                                     gene
                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                  therapy; vaccine;
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                                                                                                                                                                                                                                                                                                                 0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                     metastasis;
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2000US-0235836.
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2000US-0232397.
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2000US-0218290
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2000US-0229343
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2000US-0228924
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17-NOV-2000;
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2000US-0246611.
                                                                        GENOME
                                                                          SCI INC
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                           metastasis
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Disclosure; SEQ ID NO 21966; 3071pp + Sequence Listing; English.

expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK5492 to AAK54950 and AAM62169 represent sequences used in the exemplification of the present invention. amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis a treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased to AAK64702 encode e the human immune/haematopoietic antigen in AAM82170 to AAM91921. (I) have cytosta cytostatic and

Sequence 7016 BP; 1339 A; 2079 C; 2321 G; 1277 T; 0 other;

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Matches 21
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Вþ RESULT 3019 GCCATGGCGGTTCGGCCAGCCACCAC 2994 15

AAK70464 standard; DNA; 7016

AAK70464;

06-NOV-2001 (first entry)

Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 25276.

cytostatic; Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; gene therapy; vaccine; metastasis; ds

WO200157182-A2

09-AUG-2001

17-JAN-2001; 2001WO-US01354

18-APR-2000; 19-MAY-2000; 07-JUN-2000; 28-JUN-2000; 30-JUN-2000; 07-JUL-2000; 31-JAN-2000; 04-FEB-2000; 24-FEB-2000; 02-MAR-2000; 16-MAR-2000; 17-MAR-2000; 07-JUL-2000; 11-JUL-2000; 2000US-0179065.
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2000US-0216847.
2000US-0216847.
2000US-02174876.

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08-NOV-2000
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis at treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to polynucleotides may be used to product in (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent,
                                                                                                                                                                                                                                                                                                         Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis \dot{\ }
                                                                                                                                                                                                                                                                   Disclosure;
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CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703 CC sequences from the present invention. AAK64942 to AAK95950 and AAM82169 CC represent sequences used in the exemplification of the present invention. AX SQ Sequence 7016 BP; 1339 A; 2079 C; 2321 G; 1277 T; 0 other; SQ Sequence 7016 BP; 1339 A; 2079 C; 2321 G; 1277 T; 0 other; SQ Sequence 7016 BP; 1339 A; 2079 C; 2321 G; 1277 T; 0 other; SQ Sequence 7016 BP; 1339 A; 2079 C; 2321 G; 1277 T; 0 other; SQ SQ Sequence 7016 BP; 1339 A; 2079 C; 2321 G; 1277 T; 0 other; SQ SQ Squence 7016 BP; 1339 A; 2079 C; 2321 G; 1277 T; 0 other; SQ SQ Squence 7016 BP; 1339 A; 2079 C; 2321 G; 1277 T; 0 other; SQ SQ Squence 7016 BP; 1339 A; 2079 C; 2321 G; 1277 T; 0 other; SQ Squence 7016 BP

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AE009102 Agrobacte
AL359152 Streptomy
AL663032 Mus muscu
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AC106098 Rattus no

ALIGNMENTS

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DEFINITION
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ORGANISM
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                                                                                                                                                                                         synthetic construct.
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Orgyia pseudotsugata single capsid nuclear polyhedrosis virus
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bread wheat
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Sequence 1 from Patent WO0202785.
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                                                                                                                Dept. of Agricultural Chemistry Oregon State University
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                                                                                                 Corvallis, Oregon 97331-6502
                                                                                                                                                             George F. Rohrmann
                                                                                                                                                                                  Submitted (28-SEP-1992) to DDBJ by:
                                                                                                                                                                                                                                         pseudotsugata is localized to cytoplasmic inclusion bodies
                                                                                                                                                                                                                                                                                                       Gross, C.H., Wolgamot, G.M., Russell, R.L., Pearson, M.N. and
                                                                                                                                                                                                                                                                                                                                                                Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
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                   rohrmann@cgrb.orst.edu 503-737-0497.
                                                             503-737-1793
Location/Qualifiers
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Pred. No. 0.84;
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Pred. No. 0.
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                                                                                                 Ahrens,C.H., Carlson,C. and Rohrmann,G.F. Identification, sequence, and transcriptional analysis of lef-3, a gene essential for Orgyia pseudotsugata baculovirus DNA replication Virology 210 (2), 372-382 (1995)
                                                                                                                                                                                                                        A 37-kilodalton glycoprotein from a baculovirus of Orgyla pseudotsugata is localized to cytoplasmic inclusion bodies J. Virol. 67 (1), 469-475 (1993)
                                                                                                                                                                                                                                                                                                                                                                                          Orgyia pseudotsugata single capsid nuclear polyhedrosis virus
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    pseudosugata
                                                                                                                                                                                                                                                                                                         Gross, C.H., Wolgamot, G.M., Russell, R.L., Pearson, M.N. and
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                   Ahrens, C.H. and Rohrmann, G.F. The DNA polymerase and helicase genes of a baculovirus of Orgyia
                                                                                                                                                                                                                                                                                                                                                      Nucleopolyhedrovirus.
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a 462 c 444 g 231 t
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/db_xref="taxon:10450"
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REVLPHTLCGAAANDRHALFGDKSGMDEPFHNWRPDVLYVNRYQRAHSFNVHFCPTAV
HEPSYFEVYVTKFTWDRRSPVTWNELEYIGGNGSGLVPNPGDAFCASGQLYSIPYSVP
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/protein_id="BAA02565.1"
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/protein_id="BAA02566.1"
/db_xref="G1:222202"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agricultural Chemistry, Oregon 97331-7301, USA
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                 1218
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                                                                                                                                                                                                                                                                                    IDPDAMPALIVOFFSÖLTGRNTTHNINYRYDYNVGGALLFQDFPQDFPQFYPYGQYWPQO
PPQPFPDQPQDCPQDPQQPPQDPPQDPPQDPPQDPPQDLALVQQIELSVD
EVRELOALQLUMQQOTITWSHF AFTGTMTRILOTRVVNSAFILGAIEALQNVDRLTN
YDFNEFLRCVANETALRFEIAPDLCRVVAAFIQFFQXTHMVVXRTTFFYYNSQSLTAS
AEALHLVIVKLEWFESKIYVVWRAEEVYTNSTALAATIEELXRAVBAFIPVAAQNSAE
LAQLIAAEMRALRTVTADLQCMEDSAEDGRLQAANARYEAADANKSRELDOQLVRLRFLAA
QSETLRFEKSELATENERLGCHEDSAEDGRLQAANARYEAADANKSRELDOQLVRLRFLAA
ACONLYMAQKONEYATKTQQAAADYVAKLNAEREAXERNLRAKEDGLGATIQREQEN
AEONLYMAQKONEYATKTQQAAADYVAKLNAEREAXERNLRAKEDGLGATIQREQEN
                                                                               complement(3062. .3066)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KYFGVDANKRDVENFQLMTLSQYYLGDAKVDLMWQTMYEMYNNKQLGTIKYNVQDCL
LPIRLENKLKLTDFMYSQCIMYRLCTDDFICNISHLISSTFFHLALTNTRADPATGLT
VSDPYFFNKDDLGLMSSKGSAGLTTGKSRLFRRRIPLKDVPATAIRLGAIDENVKYBG
GKVLQPRAGVYEFAFSLDFNSLYLTIMIDICACLTNLILCEDGNVYLNDKQAINVQL
LQLLKQRSELKKCRDSQTESEFLYDLYDQMQMLSKRTANSIYGYYGIFCKLLANHIT
RVGREKLTAAIGTVEGLSNDPDLLREFGLSTLTFKVLYGDTDSTFVLPVFRREEIPEE
GRMATLGRICAAVEARVNGLFTNGYKMAFENLMSVLILLKKKKYCYINNNNKIVFKGW
/note="for DNA polymerase/ORF 65 gene" 1481 c 1514 g 1175 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence that encodes for the 
acids of ORF66 not shown here*
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVKKDMPVFMRVAFRAAIEQVLRHQDLSKCLDSLKANMLMYLDAFGITKPLTDYSFSM
TYNDGAGKTAADDDEAAPPKRRVITVARHCREILVNKATDFVPGNGDRIPYVLLDMQG
NVTQKAYPLRLFDAQTMRISWLKHMTILNTFMNELLEIFGDEHKDALAECYSAILEKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFCNAQLGGRLAQFYFVMKMDLYSYKPCHNSHIFATCRNRCSSYNTFVAPGVKNYYMD
KINVIKRKRNGSSFGEKTMALDKFLHANRVHMOTPVLEGTYLÆFRRAQRCRNGVAD
DARPFALERFSDDFEYLDSTILTINIAPVMACYDLETHSDGHNSKFBEDVIMCIGLA
VFKNDRFEKVCFVYHSEAVEIPQASDDTYVVVENNENHMITAFFEFLKTVNDDVYLDA
VGDVFDLPYIRGRLKGDKPLLÆRYDLPAMOPNTKLFITKIGNRTDTYYENYYHHIDLY
                                                                                                              LKSLKEAKL'
                                                                                                                                   DNVTLSETCTQQLKSLRDDLNKNMSNVDAINDLVKTTPELDKQAIQDVRTELSKTQSR
                                                                                                                                                                  LSQNLNDLQFGLASEQRLALEQWFSTLRETTAPNDVLNFAALTNVNDLVNDLKSOIIT
KIPANMLRTFDNRIVKPEEAGAVDNVTLISAVSRLVDEYSRLGLENAQLESTNKTLYD
                                                                                                                                                                                                                                AELRSTLDNRNREFAQGSDQFAAVNMQLNEARRAVAEKNGQLVAANEIRARLEQQLAD
ATQQLAKTEQLLVQQQKSGPMETDKQEINKEESDYLLTALDIMYKNARILNPNLGGRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with the sequence reported for the OpMNPV lef-3 gene: GenBank Accession Number D43397, which contains the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2968.
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/protein_id="AAB04046.1"
/db_xxef="GI:1063688"
/translation="MKILITYNQLQEAFRDYAPRDFAVSRDDAFRYMRIYYNEGGGNLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"ORF 65; essential for OPMNPV DNA replication; contains a number of motifs conserved among the members of the superfamily of DNA polymerases; this sequence overlaps the sequence reported for the OPMNPV gp37 gene: GenBank
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/note="submitter's given name: Orgyia pseudotsugata
/nultinucleocapsid nuclear polyhedrosis virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAB04047.1"
/db_xref="GI:1063689"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MQHQAYDKKRAALYKIATKRKAPSASDASGKRARKGAAPSDDESGSSEDEDAPCEPKC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MQRDLLSTINSMSARIKALERYEHALREIHKVIVVMRPGFNLQV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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OPU75930/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Oct 26, 2000 this sequence version replaced gi:2934903. similar to Autographa californica nuclear polyhedrosis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (06-MAR-1998) Oregon State University, Chemistry, Corvallis, OR 97331-7301, USA Sequence update by submitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (26-OCT-2000) Oregon State University, Agricultural Chemistry, Corvallis, OR 97331-7301, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  υνυ/5930 131995 bp DNA circular VRL 26-OCT-:
Orgyia pseudotsugata nuclear polyhedrosis virus complete genome
U75930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ACMNPV) complete genome: GenBank Accession Number L22858.
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Virology 229 (2), 381-399 (1997)
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                                                                                                                                                                   /product="protein kinase 1"
/protein_id="AAC59000.1"
/protein_id="AAC59000.1"
/db_xref="G:1911247"
/td_xref="G:1911247"
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RKTIAAHSF$ADEINVHDLMSDHPSFVDMYFCYSSPFAWAIVMDYVPCPDLFEFTLQTQ
GALDNALVVNIVRQLCDALNDLHNATGYIHNDVKLENVLYFGARDRVYLCDYGLCKRE
HSPVHHGTLEYFSPEKIRRHNYARSFDMYANGVLAYKLLTGGRHPFERSADEYLDLAS
                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10450"
complement(123. .947)
                         /codon_start=1
/product="1629-capsid"
/protein_id="AAC59001.1"
/db_xref="GI:2934904"
                                                                                                                                                      MRRRQQYNDPAALKNVRNLMARDFVFCLTRFNFECRSTDYKQIAKHSFLASRHDYI"
                                                                                                                                                                                                                                                                                                                                                                                                                       polyhedrosis virus"
translation="MMERQYQSVRSYLINNQHNAIAAGPFLQRVAGPEAHSVGRNVGD/
                                                                                                             /note="ORF2; Acmnpy ORF9 homolog"
                                                                                                                                                                                                                                                                                                                                 /note="ORF1; pk-1, ACMNPV ORF10 homolog
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Orgyia pseudotsugata single capsid nuclear
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82.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MGASQNSEOKILKLEYRWSSQTGAALDDEKDLHCLYDLEREVGA
HINKRADDKARKKCAEKAALKRVEIAADRHMLEAAAAPACADDGRWSTLSRAQLDDI
AREKEIVDRIHRLQLKQDSLLKQDRLKKR"
complement(4125. .4739)
/note="ORF6; lef-2, AcmnPV ORF6 homolog"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MPDYSYRPTIGRTYVYDNKYYKNIGSVIKNAKRKKHLLEHEEDE
KHLDPLDHYMVAEDPFLGPGKNQKLTLFKEIRNVKPDTMKLIVNWSGKEFLRETWTRF
VEDSFPIVNDQEVMDYFLVVNNRPTRPNRCYKFLAQHALRWDCDYVPHEVIRIVEPSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="polyhedrin"
/protein_id="AAC59002.1"
/db_xref="GI:1911249"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(2533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KRRPAVEHTDGNSTGNNSDDWRDD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKTLKKLRKIEDQSSTQTLLKDVDTTDKTKTILKNFVTNIDRISKQEQEEKDRLDTIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mrknngasqypehlttvhkrhrlqlscvwcddqrswdphsakgl
mfehmfcclrlyvqqkikh"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="ORF3; ph, AcmnPV ORF8 homolog"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="late expression factor 2"
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/protein_id="AAC59005.1"
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PCMSKTMADLSSAPRGNMYRKRFEFNCYLANVITCTKCKTACLIGALLHFYRNDAKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="unknown"
/protein_id="AAC59004.1"
/db_xref="GI:1911251"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(3698. .4093)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EILIEVSLVFKVKEFAPDAPLFTGPAY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGMNNEYRISLAKKGGGCPIMNIHAEYTNSFESFVNRVIWENFYKPIVYIGTDSSEEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAC59003.1"
/db_xref="GI:1911250"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="ORF4"
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PIRHALGLPVGDHIHVYCEAAPTCAALPNAMPALYDYMVRRIGEGKRVLVHCYAGASR
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IARYILAECGAVLVIDHPLDVFGETEEGVNELLEVQRINAGGDL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(4742. .4975)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="ORF5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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/db_xref="GI:1911255"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="ORF7;
                                                                                                                                                                                                                                                   complement(5669. .6151)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                       /note="ORF9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="ORF8;
                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                   ptp-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACMNPV ORF5 homolog"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACMNPV ORF4 homolog"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .3541)
                                            Query Match
Best Local
                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
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                                                      Similarity
                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MSLSKLLVYAYYGSYNLPHDRYGESYHLYRIVHEHLTNTYVSN
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DPDIRADGWYHKFCVLTYMHLVACGAVPAGSATRLRDAVAKHIGPNDEGNCAFAIAA
VYGRFCAIGREHFAHKTACMHILFQFMRNDLTPADERHPCFGVIKDFGRQCKDTYTD
LETHADALYIHGTTDRQKNALFDLLCCVNASDIDADCYDCVVNKFYATQNKKYKM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(8180..9142)
/note="ORF12; ACMNPV ORF13 homolog"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref "GI:1911256"
/tianslation="MLTSRRWAVIYIRTSERNCGGAWCTNGVRRRRQVHLPSVRARAM/tianslation="MLTSRRWAVIYIRTSERNCGGAWCTNGVRRRRQVHLPSVRARAM/fieddayifeddayifeddayifeddayifeddayifeddayifeddayifedayifeddayifeddayifaryyddayifer
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/note="ORF10; ptp-1, ACMNPV ORF1 homolog"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="late expression factor 1"
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EGKEDAVQRIMFSGNRGFHLMLKFCGKFKMDAPKSLREHWFNVFKQPAKLVSGDIRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(9094.
/note="ORF13; le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVTKHPHLAVFMGRVEDRGVTQIAFARGQEEHFRKRKLEFEEGMDVDVRGRAPNPLLA
VHCIKEEFANGGHKIRRLPKKYIEVDCAVNVAKDIVKKAILNKT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAQPDSLGSLFATKHGLVQLLQQFSFÄNKNEVLLAVGÄNKDHDRDNLLDK IEAVLNHV
KTLNTNSDKFISAHKSFKLEVGARFEQFEQRLQTLDTKLNALQCAAPTETAPGVVFPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mfswmfgwwnaadeqvnaefdeqayrryavdqrahsdlvrrdvf
RCHPFVFKFRYVLDETAGRCCSVVDFCKGLKISHDLLQRCNFDRQHVRQLNELVLGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6819. .7814
/note="ORF11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HWTHGLNRSGYLVCRYMVERLGVSPTDAIARFETARGHKIERTNYLQDLLARKHVRGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="protein tyrosine phosphatase 1"
/protein_id="AAC59009.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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APGYGLAENFERRRAVARHPLHYPTFGAAALTRRGGALSEWRLLNEFELLARRSDELL
KQQFGKSTPTIRQLRDNVQLLLLNLHPVYDNNRFVPPSVQYLGGGLHLAQALFQRLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TQQLQQRIKACSAGCLAGGTPPTSK" 9893. .11362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAC59011.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAC59010.1"
/db_xref="GI:1911257"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFADCVRRAVHMY IGDAREDLVLRYWPDVDRDVFCNANKQIRAPFSYNYKGGDYSRC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                       PLERRLNESYDGAYYYSFGSGIDTNSIHAEFLOMLLDTFANLNNYTVLMKYDDAYAAS
VALFRNYLAOKWFSOTAYLRHKNYVAFYTOAGLOSSDEALQARVPMYCLPMMGDOFHH
ARKLOOFGVARALDTAAVSAPOLOLAIREVIADGEAYRARIDKLRAVVEHDAAPDEKA
VKFTERVIKENNDVNWPARSLKTTAANMAYSDYFVRFPL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="ecdysteroid UDP-glucosyltransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="ORF14; egt, AcMNPV ORF15 homolog"
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                                                                                                                                                                      /protein_id="AAC59014.1"
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                                                                                                                                                                                                                                                                                                    /note="ORF15;
                                                                                                                                                                                                                                       /product="unknown"
                                                                                                                                                                                                                                                                    /codon_start=1
                                                      82.8%;
                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACMNPV ORF11 homolog"
                                                      Pred. No. 2e+02;
                                                                                Score 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lef-1,
                                                                                                                                                                                                                                                                                                    ACMNPV ORF16 homolog"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .9825)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACMNPV ORF14 homolog"
                                                                                   DB 14; Length 131995;
                            5
                            Indels
                                0;
                                Gaps
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FEATURES
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                                                                                                                                                 source
                                                                                                                                                                                                  of Bibb et al., Gene 30:157-66(1984) as implemented at the http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we arrange for a small overlap between neighbouring submissions. Cosmid 7H1 lies between 10A5 and 7B7 on the AseI-B genomic restriction fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 cacgcaaaggcgcgtcggccagccacgac 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the Frameplot program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (20-JAN-1998) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 70H, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Details of S. coelicolor sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces coelicolor sequencing at The Sanger Centre is funded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murphy, L. and Harris, D. Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A set of ordered cosmids and a detailed genetic and physical map for the 8 mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oxidoreductase; peptidylprolyl isomerase; sigma factor; transferase; xlnA; xylanase A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  abfB; aminotransferase; arabinofuranosidase; cbiM; cbiN; cbiO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces coelicolor cosmid 7H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kinashi, H. and Hopwood, D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinomycetales; Streptomycineae; Streptomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cbiQ; chitinase; cobalt transport system; export protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL021411.1 GI:2808758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bases 1 to 35654)
                                     /organism="Streptomyces coelicolor A3(2)"
/strain="A3(2)"
                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                 .35654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35654 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
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                                                                                                                                 /gene="SC7H1.03c"
/note="SC7H1.03c"
/note="SC7H1.03c, unknown, possible membrane protein, 391 aa; contains PS00213 Lipocalin signature, though that the spurious of the second se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="arabinofuranosidase"
/product="arabinofuranosidase"
/product="arabinofuranosidase"
/product="GAA16189.1"
/db_xref="GI:2808760"
/db_xref="GI:2808760"
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/db_xref="SHISS-PROT:054161"
/translation="MHRGSLSRGHTSAVLAAVVAALAALLVATTPAQAAGSGALR
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/GAGSNRCLDVLGGSQDARANGANAVQANAPTLFYFARKNIWYLAYQNGSWPEI
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//GAGSNCSGNAMNGANAPTLFYFARKNIWYLAYQNGSWPEI
//GAGSNCSGNAMNGANAPTLFYFARKNIWYLAYQNGSWPEI
//GAGSNCSGNAMNGANAPTLFYFARKNIWYLAYQNGSWPEI
//GAGSNCSGNAMNGANAPTLFYFARKNIWYLAYQNGSWPEI
//GAGSNCSGNAMNGANAPTLFYFARKNIWYLAYQNGSWPEI
//GAGSNCSGNAMNGANAPTLFYFARKNIWYLAYGNGHAWANAPTLFYFARKNIWYLAYGNGSMAMNGANAPTLFYFARKNIWYLAYGNGSMAMNGANAPTLFYFARKNIWYLAYGNGSMAMNGANAPTLFYFARKNIWYLAYGNGSMAMNGANAPTLFYFARKNIWYLAYGNGSMAMNGANAPTLFYFARKNIWYLAYGNGSMAMNGANAPTLFYFARKNIWYLAYGNGSMAMNGANAPTLFYFARKNIWYLAYGNGSMAMNGANAPTLFYFARKNIWYLAYGNGSMAMNGANAPTLFYFARKNIWYLAYGNGSMAMNGANAPTLFYFARKNIWYLAYGNGSMAMNGANAPTLFYFARKNIWYLAYGNGSMAMNGANAPTLFYFARKNIWYLAYGNGSMAMNGANAPTLFYFARKNIWYLAYGNGSMAMNGANAPTLFYFARKNIWYLAYGNGSMAMNGANAPTLFYFARKNIWYLAYGNGSMAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YRTSSDPTDPNGWSAPQPLFTGSISGSDTGPIDQTLIADGQNMYLFFAGDNGKIYRAS
MPIONFPGNEGSSYTTIMSDTKANLFEGVQVYKVQGQNQYLMIVEAMGANGRYFRSFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EMBL:M64551) arabinofuranosidase precursor (EC 3.2.1.55)(alpha-1-arabinofuranosidase) (arabinosidase) (478 aa), fasta scores; opt: 3129 z-score: 1807.5 E():
/product="hypothetical protein SC7H1.03c"
                                                                                                                                                                                                                                                                                                                                                                    /gene="SC7H1.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGKSPNAGGDYNSLPWRPGVLTLRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        signal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="SC7H1.02, abfB, arabinofuranosidase precursor, len:
475 aa; almost identical to S. lividans TR:P96463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="SC7H1.01c, xlnA, xylanase A precursor, partial CDS, len >147 aa; almost identical to S. lividans XYNA_STRLI P26514 endo-1,4-beta-xylanase a precursor (ec 3.2.1.8) (XYLANASE A) (477 aa), fasta scores; opt: 926 z-score: 1591.1 E(): 0, 97.9% identity in 146 aa overlap. Contains N-terminal signal sequence and Pfam match to entry
                                                           /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {	t ASSLSGSWTPQAASEGNPFAGKANSGATWTNDISHGDLVRDNPDQTMTVDPCNLQFLY}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.8% identity in 477 aa overlap. Contains N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  832. .2259
                                                                                                           'codon_start≈1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A precursor (xlnA) genes from: 166 to: 2759"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSADRVYNWAVQNGKQVRGHTLAWHSQQPGWMQSLSGSALRQAMI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLGAAAAQSGRYFGTAIASGRLSDSTYTSIAGREFNMVTAENEMKIDATEPQRGQFNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="xylanase A"
/protein_id="CAA16188.1"
/db_xref="GI:2808759"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycosyl_hydro3 PF00331, Glycosyl hydrolases family 10,
score 107.60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(<1. .441)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycosyl hydrolases
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/gene="xlnA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="abfB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="SPTREMBL:054160"
/translation="MGSYALPRSGYRRSIRVLLLALVVGVLGTATALIAPPGAHAAES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="xlnA'
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slycosyl hydrolases family 10, from 1 to 71, score 107.60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transl_table=11/
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.2259
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(abfB) and xylanase

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protein, len: though this

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Db 31687 GCCAAGGCGCGTCGTCCATCCACGA 31663
                                                                                                                                                                   Query Match
                                                                                                                Matches
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                                                      4 gcaaaggcgcgtcggccagccacga 28
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                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="SC7H1.05"
4245. .5138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SC7H1.04"
3646. .4248
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EPVQQDKLVGGDIYDVAATPWGTRVLIGDVQGKGLPAIGMAIDVVGAFREAAHREPTV
TALVDSLEAAVVRHNGYAEQRGEPERFVTAVVLGVDTGAETQLVTCGHIPPYLLHUGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="msrpsraapapaedgadgdgisirtpptrvvalvtvaatvvtv
vLgavtgtavLLigLLvfLpapasaLctprQttLvsAmvsIvvIvpvaLsteQLadrv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(3050
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/db_xref="GI:2808761"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="Sptrembl:054164"
/translation="MNDPOGVPAAPSDRDLPNHRRTREELLMKIGPENNGTPSRRRWA
/translation="MNDPOGVPAAPSDRDLPNHRRTREELLMKIGPENNGTPSRRRWA
/translation="MNDPOGVPAAPSDRDLPNHRRTREELLMKIGPANSTPAPSPSASSS
| RWGVPLGVATGVTAMSVAAVVVLGGSGSAGPGAADPAHGGADPANSTPAPSPSASSS
| PGGTSPEADDTVDATTPPIDAGTATRILSSCLGADASRYHAVVAVWTPLATEDWDGV
| VAYDSAGQYVQCQSKGDKGTSQDSPPTFINDRLWGTGRIVEYFDSMLMPAGEGKYLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MSDRELWARAADGDREAFGRIFDRHGKAYYNHLFRRTADWSEAE
DLTSTVFLHAWRRRADTVLDRDSALPWLLGIANGQLSNTRRRLRRAEALLHRLVSHEE
SVGDHADRVAGRIDDERRMSEIHRALARLPRHEREVVELCVWSGLDQQAAAAVLKVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(3426.
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/note="percentage"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {f vTAVGAGTEHAPLGLADLVDEPRTVSWFPFPAGATLLLCTDGLTEARSPAGAFYPLET}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative sigma factor"
/protein_id="CAA16191.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="PS00213 Lipocalin signature"
                                                                                                                                                                                                                                                                                                  complement(5122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="hypothetical protein SC7H1.05"
/protein_id="CAA16192.1"
/db_xref="GI:2808763"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="SC7H1.04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTYKSRLHRARRRLGADLGGAAAPPPFSSRNPVNEKEVAR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="SC7H1.04"
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                                                                                                                                                                                                                                                                                                                                                                 complement(5122. .5283)
                                                                                                                                                                                                                                                                                                                                                                                           YDASGREIYNQAEDPKFTDEQ"
                                                                                                                                                                                                                                                                                                                                                                                                                     LGAGHYSSDVAKITVSYGEDPKQYPARMADGAFVYGAALSPDTPPGPRYTGPSPYVHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="possible RBS upstream of SC7H1.05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:054163"
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                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                    /gene="SC7H1.06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="SC7H1.05, unknown, len: 297 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="SC7H1.05"
                                                                                                                                                                                                                                                       note="SC7H1.06, unknown, len: 53 aa"
                                                                                                                                         69.7%;
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                                                                                                          0;
                                                                                                                                                                      Score 20.2;
                                                                                                                                               Pred. No.
                                                                                                                     Mismatches
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                                                                                                                                                                      DB 1; Length 35654;
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AC106098/c

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REFERENCE
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AUTHORS
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Contact: hgsc-help@bcm.tmc.edu
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Consensus quality: 126356 bases at least Q40 Consensus quality: 135615 bases at least Q30 Consensus quality: 142780 bases at least Q20
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 74 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 19 Row: g Column: 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garc
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis isolate DS13 unknown sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muzny, D.M., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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Comparing genomes within the species Mycobacterium tuberculosis
                             Small, P.M.
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                                               Mycobacterium; Mycobacterium tuberculosis complex. 1 (bases 1 to 4926)
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/protein_id="AAH11138.1"
/db_xref="GI:15029830"
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/clone_lib="NIH_MGC_10"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Small, P.M., Kato-Maeda, M., Rhee, J.T., Gingeras, T.R., Salamon, H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (13-FEB-1998) Osamu Ohara, Kazusa DNA Research Institute, DNA Technology; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens mRNA for KIAA0589 protein, partial cds
                                                                                                                                                                                                                                                                                                                            98290545
                                                                                                                                                                                                                                                                                                                                                                                Nomura,N. and Ohara,O. prediction of the coding sequences of unidentified human genes. IX. The complete sequences of 100 new cDNA clones from brain which can
                                                                                                                                                                                                                                                                                                                                                                                                                                           Nagase, T., Ishikawa, K., Miyajima, N., Tanaka, A., Kotani, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax:+81-438-52-3914)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 5047)
Ohara,O., Nagase,T. and Ishikawa,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plus clone:HJ2695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens male brain cDNA to mRNA, clone_lib:pBluescriptII SK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIAA0589 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB011161.1 GI:3043701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AB011161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 4926)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                             large proteins in vitro 5 (1), 31-39 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="sequence found to be deleted in some clinical
isolates"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mycobacterium tuberculosis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="H37kv"
/product="KIAA0589 protein"
/protein_id="BAA25515.1"
/db_xref="GI:3043702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:1773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /isolate="DS13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                      /clone="HJ2695"
                                                                  /codon_start=1
                                                                                                                      /gene="KIAA0589"
                                                                                                                                                                /tissue_type="brain"
/clone_lib="pBluescriptII SK plus"
                                                                                                                                                                                                          /sex="male"
                                                                                                                                                                                                                                             /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                 /gene="KIAA0589"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1473 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.3%;
91.3%;
                                                                                                                                                 2064
                                                                                                                                                                                                                                                                                         504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 19.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. le+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                909 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 4926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                      Notes:

Notes:

Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhillesanger.ac.uk
On Jun 27, 1998 this sequence version replaced qi:1449358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cole, S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E., Tekaia, F., Badcock, K., Basham, D., Brown, D., Chillingworth, T., Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S., Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J., Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M.A., Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Seeger, K., Skelton, S., Connocial Manager, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Connocial M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Connocial M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Connocial M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Connocial M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Connocial M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Connocial M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Connocial M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Connocial M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Connocial M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Connocial M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Connocial M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Connocial M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Connocial M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Connocial M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Connocial M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Connocial M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Connocial M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Connocial M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Connocial M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Connocial M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Connocial M.A., Rogers, J., Rutter, S., Seeger, R., Skelton, S., Connocial M.A., Rogers, J., Rutter, S., Rutter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Squares, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parkhill,J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complete genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium; Mycobacterium tuberculosis complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis H37Rv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis H37Rv complete genome; segment 145/162.
277165 AL123456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jun 27, 1998 this sequence version replaced gi:1449358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 33818)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 33818)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        965 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL123456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   393 (6685), 537-544 (1998)
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KLLPGYYMNLNQNPRTLLPKEYGLYCVQSGGKNIRVVVMNNILPRVVKMHLKFDLKGS
TYKRRASKKEKEKSFPTYKDLDFMQDKDFEDELLLDADFUXLQRDCTLYLESFKIM
DYSLLLGVHNLDQHERERQAGGAQSTSDEKRPYGQKALYSTAMESIQGAARGEAIES
DDTMGGIPAVNGRGERLLLHIGIIDILQSYRFIKKLEHTWKALVHDGDTVSYHRDSFY
AERFFKEMSNIYFRKNJSLKSSPSKKGRGGALLAVKFLGPTAAFSAQIPSEREEAQY
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RYRRKTQSSGQDGRPQEEPPAEEDLQQITVQVEPACSVEIVVPKEEDAGVEASPAGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QLGIGYTVGHLSSKPERDVLMQDFYVVESIFFPSEGSNLTPAHHFQDFRFKTYAPVAF
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ESGAAAGLAXKAAPTEVLSMTAQPGPGHGKKLGHRGVDASGETTYKKTTSSTLKGAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.3%;
91.3%;
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Where possible we choose an initiation codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1480 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33818 bp
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REFERENCE

KEYWORDS

ORGANISM

VERSION ACCESSION DEFINITION 밁 δ

Matches

MTCY78/c

BASE COUNT ORIGIN

COMMENT

REFERENCE

AUTHORS

JOURNAL

JOURNAL MEDLINE

TITLE

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FEATURES
                                                                                                                                                            CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 initiation codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="guaA"
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/product="guaA"
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/db_xref="Gi:1449391"
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/db_xref="SWISS-PROT:050729"
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APVAAFEAFDRRLAGVQYHPEVMHTPHGQQVLSRFLHDFAGLGAQWTPANIANALIEQ
VRTQIGDGHAICGLSGGVDSAVAAALVQRAIGDRLTCVEVDHGLLRAGERAQVQRDFV
AATGANLVTVDAAETFLEALSGVSAVBEGKKIIGRGFIAFEGAVRDVLDGKTAEFILV
QGTLYEDVVESGGGSGTANIKSHHNVGGLDDDLKFTLVEPLRLLFKDEVRAVGRELGL
PEEIVARQPFPGFGLGIRIVGEVTAKRLDTLRHADSIVREELTAAGLDNOIWQCDVVL
LADVRSVGVQGDGRTYGHPIVLRPVSSEDAMTADWTRVPYEVLERISTRITNEVAEVN
/note="Rv3398c, (MTCY78.30), len: 359, GGPP synthetase, most similar to AE000797_3 Methanobacterium thermoautotrop 026156 bifunctional short chain isoprenyl diphosphate
                                                                                                                 /gene="idsA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="SWISS-PROT:050728"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Rv3397c, (MTCY78.31), len: 302, phytoene synthase, similar to many, e.g. PSY2_LYCES P37273 phytoene synthase 2precursor (310 aa) Fasta scores, opt: 421, z-score: 500.0,E(): 6.6e-21, (32.9% identity in 295 aa overlap);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1428. .1463)
/gene="guah"
                                                                                                                                                                                     complement(2673.
/gene="idsA"
                                                                                                                                                                                                                                                                                                                     complement(2108. .2185)
/gene="phyA"
                                                                                                                                                                                                                                                                                                                                                                                     AALASSVTCGPAHGPLPADLGSHPSH"
                                                                                                                                                                                                                                                                                                                                                                                                              TNILRDVREDFLNGRIYLPRDELDRLGVRLRLDDTGALDDPDGRLAALLRFSADRAAD
WYSLGLRLIPHLDRRSAACCAAMSGIYRRQLALIRASPAVVYDRRISLSGLKKAQVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="phyA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          containsPS01045 Squalene and phytoene synthases 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(1736. .2644)
/gene="phyA"
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/gene="phyA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVVLDITSKPPATIEWE"
                                                                                                                                                                                                                                                                              note="PS01045 Squalene and phytoene synthases signature
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/clone="Y78"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transl_table=11
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="Rv3399"
3775. .4821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="CAB01025.1"
/db_xref="GI:1449389"
/db_xref="SWISS-PROT:Q50727"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y09T_MYCLE (261 aa) Fastascore, opt: 1293, z-score: 1478.0, E(): 0, (74.4% identityin262 aa overlap), also similar to wmCY39.11c (34.9% identityin 238 aa overlap); Rv3400 and Rv3401 are similar to beginning and end of mCY39.11c with approx. 270aa missing fromthe middle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Rv3400, (MTCY78.28c), len: 262, possible BETA-PHOSPHOGLUCOMUTAGE, similar toseveral, e.g. (9: PGMB_BACSU PUTATIVEBETA-PHOSPHOGLUCOMUTAGE (226 aa, E(): 1.5e-05, 33.9% identity in 245 aa overlap), also highly similar to U00015_17 Mycobacterium leprae cosmid B1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="Rv3400"
4885. .5673
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ARIGIPDRPAAELQDLAHYIVDRQA"
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LVHNFSLVHDDLMDRDEHRRHRPTVWALWGDAMALLAGDAMLSLAHEVLLDCDSPHVG
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RTDNDTWDLASSVGATATMIATARALASRAENPLINDPFAEPLVRAVGIDLFTRLASG
ELRLEDIGDHATGGRWMIDNIAIRTKFYDDFFGDATTAGIRQVVILAAGLDTRAVRLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="hypothetical protein Rv3399"
/protein_id="CAB01024.1"
/db_xref="SWISS-PROT:Q50726"
/db_xref="SWISS-PROT:Q50726"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AALRAISEATRELIRGQAADTAFESRTDVALDECLKMAEGKTAALMAASAEVGALLAG
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/note="Rv3401, (MTCY78.27c), len: 786, unknown, similar tomany hypothetical proteins, e.g. YVDK_BACSU HYPOTHETICAL
                                                                                                                                                                                                                               GVAAGRAGNFAVVVGINRTGRAAQAAQLRRHGADVVVTDLAELL"
                                                                                                                                                                                                                                                              DDPGAAETVYGLGNRKNDMLHKLLRDDGAQVFDGSRRYLEAVTAAGLGVAVVSSSANT
RDVLATTGLDRFVQQRVDGVTLREEHIAGKPAPDSFLRAAELLGVTPDAAAVFEDALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="hypothetical protein Rv3400"
/protein_id="CAB01023.1"
/db_xref="GI:1449387"
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PTAFSAEGLLSYLPPQGQDRLLDAITALSAPDSRLATQSPLVLDLAEEDEKKMRWKSA
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                                                                                                                                                                                                                                                                                                                                                WKAMFDAYLAERAERTGEKFVPFDPAADYHTYVDGKKREDGVRSFLSSRAIEIPDGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
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                                                                                                                                                /gene="Rv3401"
                                                                                                                                                                                                                                                                                                                                                                                /db_xref="SWISS-PROT:Q50725"
/translation="mANWYRPNYPEVRSRVLGLPEKVRACLFDLDGVLTDTASLHTKA
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                                                                          /gene="Rv3401"
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/rpt_family="AluJ" 456. .744

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Db 30887 CGCAAAGCCGCGTCGGCCATCCA 30865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (26-AUG-1998) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA Map and sequence oriented from p telomere to centromere. Cosmid R32516 overlaps cosmid R31449 (AC005175) to the left from bases 1 to 8,571 of this accession, and is separated from cosmid F16815 (AC004637) to the right by approximately 5 kb. Additional chromosome 19 map and sequence information may be obtained at: http://www-bio.llnl.gov/bbrp/genome/genome.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lamerdin, J.E., McCready, P.M., Skowronski, E., Adamson, A.W.,
Burkhart-Schultz, K., Gordon, L., Kyle, A., Ramirez, M., Stilwagen, S.,
Phan, H., Velasco, N., Do, L., Regala, W., Terry, A., Garnes, J.,
Danganan, L., Poundstone, P., Christensen, M., Georgescu, A., Avila, J.,
Liu, S., Attix, C., Andreise, T., Trankhein, M., Amico-Keller, G.,
Coefield, J., Duarte, S., Lucas, S., Bruce, R., Thomas, P., Quan, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coefield, J., Duarte, S., Lucas, S., Bruce, R., Thomas, P., Quan, G., Kronmiller, B., Arellano, A., Montgomery, M., Ow, D., Nolan, M., Trong, S., Kobayashi, A., Olsen, A.S. and Carrano, A.V. Sequence analysis of a 3.5 Mb contig in human 19p13.3 containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 38209)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC005542.1 GI:3461801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens chromosome 19, cosmid R32516, complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC005542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to beginning and end of MTCY39.11c with approx. 270aa missing from the middle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=]
                                  /rpt_family="Alusc"
236. .286
                                                                                                                chromosomes from hybrid 5HL2-B, which carries chromosome 19 as its only human chromosome."
                                                                                                                                                                                                                                                                                                                                      /map="19p13.3 between CDC34 and D19S342"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                     /note="Cosmid library constructed at LLNL from flow-sorted
                                                                                                                                                                                                                                                                          /cell_line="5HL2-B"
                                                                                                                                                                                                                                                                                                      /clone="R32516"
                                                                                                                                                                                                                                                                                                                                                               /chromosome="19"
                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
                                                                                                                                                                                                                                                 /clone_lib="LL19NC03 R chromosome 19-specific cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
rpt_family="L1PB1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38209 bp
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repeat_region
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//note="predicted exon, program: grail2exons_human_1.3,
frame: 2, quality: excellent, score: 100.000"

complement(2694. .2856)
//note="predicted exon, program: grail2exons_human_1.3,
frame: 2, quality: excellent, score: 100.000"

complement(3741. 3886)
//note="predicted exon, program: grail2exons_human_1.3,
frame: 0, quality: excellent, score: 100.000"
                                                                                                                                                                                                                                                                                           /rpt_
11697
                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="LINE2"
complement(10187. .10279)
/rpt_family="(CGG)n"
complement(11027. .11073)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="AluJo"
9062. .9360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="LINE2"
complement(8516. .8805)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (7819.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(7302. .7579)
/note="predicted exon, program: grail2exons_human_1.3,
frame: 2, quality: excellent, score: 96.000"
complement(7478. .7538)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="AluSx"
6002. .6360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(4321...4416
/note="predicted exon,
frame: 1, quality: exce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (Join (<2487. .2603,2694. .2856,3741. .3886, 4321. .4416,7302. .>7579))
/note="Hypothetical partial protein; Most similar to YB3C_SCHPO HYPOTHETICAL 60.9 KD PROTEIN C2F12.12C IN CHROMOSOME II gnl|PID|e325370 (Z97211) hypothetical protein [Schizosaccharomyces pombe]; 5'-end of
                                                                                                                                                    complement(12660. .12847)
                                                                                                                                                                                                                          /rpt_family="Alusg"
12261. .12559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9611.
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                                                                                                                                                                                  /rpt_
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/product="R31449_3"
/protein_id="AAC32903.1"
/db_xref="GI:3461802"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical gene not discernible in genomic sequence at this time"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="AluJ"
1803. .1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="(CAG)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLLEDIQVYMELEQGKNADFWRDMTTITEDEISKLRKLEASGKGPG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="MER20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="Alusc" 745. .911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rpt_family="Alusx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="Aluy"
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                                                                                                                                                                                                                                                                                                                                                                    _family="MIR"
5, 11677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _family="LINE2"
                                                                                                             _family="AluSg/x"
                                                                                                                                                                                                                                                                                                                            _fami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _family="MLT1C"
                                           .family="AluSx"
                                                                                                                                                                                  family="AluSx"
              .13703
                                                                               .13401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality: exon, program: grail2exons_human_1.3,
t(5352, .5489)
ly="LIMPO"
                                                                                                                                                                                                                                                                                                                    y="Alusx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8275)
                                                                                                                                                                                                       repeat_region
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/rpt_family="Alusx"
20316. .20356
                                                                                                                                      /rpt_family="AluSx"
19312. .19613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPASDGESDT"
                                                                                                                                                                                                           /rpt_family
19016. .193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16162.
                                                                                              family="Aluy"
                                                                     .19790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .16753
                                                                                                                                                                                                                                        "AluSx"
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/Tpt_family="Aluy"

/note="pDS similarity to overlapping ESTs:
(13795. .1430) AA621023 agg3c09.sl Soares testis NHT Homo
sapiens cDNA clone 1056208 3'; Score: 856 Identity:
432/436 (99%).-(13795. .14267) AI018772 ov332e07.xl
Soares testis NHT Homo sapiens cDNA clone IMAGE:1639044 3'
similar to contains TAR1.t3 PTR5 repetitive element;
score: 938 Identity: 471/473 (99%).-(1460. .14100)
AA128938 zo11bl2.rl Stratagene neurospithelium NT2RAMI
37234 Homo sapiens cDNA clone 567359 5'; Score: 886
Identity: 453/459 (98%).-(14913. .14564) M94459 ze12e03.rl
Soares fetal heart NHH119W Homo sapiens cDNA clone 388780
Score: 668 Identity: 345/350 (98%).-(15439. .14978)
R33135 y960e12.rl Homo sapiens cDNA clone 36877 5'. Score:
766 Identity: 477/476 (93%).-(15444. .15189) AA323207
EST25973 Cerebellum II Homo sapiens cDNA 5' end; Score:
766 Identity: 278/284 (97%).-Additional EST matches:
AA975069, AA128939, AA524185, AA482347, H67626, H73320,
M78980, and many others. ."
complement(13798. .>37203)
/note="Encodes human homolog of mouse
phosphatidylinositol-4-phosphate 5-kinase I-gamma"
/product="Homo sapiens mRNA for KIAA0589 protein"
complement(154545. .16681)
/note="DDS similarity to overlapping ESTs:
(15842. .15645) 242707|HSCORG021 H. sapiens partial cDNA
sequence: clone c-0r902. Score: 388 Identity: 196/198
(98%).-(15884. .15653) T31546 EST34519 Homo sapiens cDNA 5'
end similar to None; Score: 448 Identity: 228/232
(98%).-(16081. .15653) AA446775 zw89066.rl Soares total
fetus Nb2HF8 9w Homo sapiens cDNA clone 784139 5'; Score:
"T20 Identity: 377/387 (97%).-"
complement(18117. .18182)
//note="predicted exon, program: grail2exons_human_1.3,
frame: 2, quality: good, score: 52.000"
complement(18733. .18853)
/note="predicted exon, program: grail2exons_human_1.3,
frame: 0, quality: good, score: 68.000"
18879. .19014
                                                                                                                                                                                                                                                                                                                                                                                                                 EDLKGSTYKRRASKKEKEKSFPTYKDLDFMQDMPEGLLLDADTFSALVKTLQRDCLVL
ESFK INDYSLLLGVHNIDQHERERQAQGAQSTSDEKRPVGQKALYSTAMESIOGGAAR
GEA IESDDTMGGIPANMGRGERLLHHIGI IDILQSYRFIKLEHTWKALVHDGDTVSV
HRPSFYAERFFKFMSNTVFRKNSSLKSSPSKKGRGGALLAVKPLGFTAASFASQIPSE
REBAQYDLRGARSYPTLEDEGRPDLLPCTPPSFEEATTASIATTLSSTSLSIPERSPS
                                                                                                                                                                                                                                                                                                                                         ETSEQPRYRRRTQSSGODGRPQEEPPAEEDLQQITVQVEPACSVEIVVPKEEDAGVEA
SPAGASAAVEVETASQASDEEGAPASQASDEEDAPATDIYFPTDERSWVYSPLHYSAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/product="KIAA0589, partial CDS"
/protein_id="AA032904.1"
/db_xref="GI:3461803"
/translation="NLNQNPRTILPKFYGLYCVQSGGKNIRVVVMNNILPRVVKMHLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="putative lipid kinase"
/note="Human homolog of mouse phosphatidylinositol-
4-phosphate 5-kinase I-gamma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(16781. .16783,17051. .17134,22498. .2263 25319. .25423,26521. .26553,26887. .26995,27701. .27865, 29588. .29672,30952. .31000,32239. .32322,35440. .35845, 36904. .>37203))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="DDS similarity to AA527155 ni07c01.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:967296; Score: 958 Identity: 546/592 (92%)."
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
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Pisani, C., Pollara, R., Vollara, R., Voll
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t, A.F.A. & Green, P. (1996-1997)
Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 156881 bases at least Q40 Consensus quality: 166139 bases at least Q30 Consensus quality: 169716 bases at least Q30 Insert size: 187000; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                           Center clone name: 383_B_15
                                                                                                                                                                                                                                                                                                                                                                              Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Insert size: 171925; sum-of-contigs
Quality coverage: 3.7 in Q20 bases; sum-of-contigs
Quality coverage: 4.0 in Q20 bases; sum-of-contigs
Quality coverage: 4.0 in Q20 bases; sum-of-contigs
**NOTE: This is a 'working draft' sequence. It currently
** consists of 38 contigs. The true order of the pieces
** is not known and their order in this sequence record is
** arbitrary. Gaps between the contigs are represented as
** runs of N, but the exact sizes of the gaps are unknown.
** This record will be updated with the finished sequence
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* as soon as it is available and the accession number will * be preserved. 17626: contig of 2371 bp in 16 17626: contig of 2371 bp in 16 17627 17766: gap of 100 bp 17727 20315: contig of 2589 bp in 16 20316 20415: gap of 100 bp 20416 21588: contig of 1173 bp in 16 21589 21688: gap of 100 bp 21689 2389 nortig of 100 bp 54010 54109: gap of 100 bp 54110 57886: contig of 3777 bp 57887 57986: gap of 100 bp 57987 53137: contig of 5151 bp 63138 63237: gap of 100 bp 63238 68261: contig of 5024 bp 68262 68361: can cf 21689 23899 26022 26122 86600 91152 91252 40457 36995 33055 29984 11605 49434 49533: gap of 49534 54009: cont 79723 79822: gap of 79823 86499: cont 44873 40557 23999 13074 13173: 1 1032: contig of 1032 bp in length 1033 1132: gap of 100 bp 1133 2147: contig of 1015 bp in length 2148 2247: gap of 100 bp 6695 6794: gap of 6795 7868: con 5050 5149: gap of 5150 6694: con 7869 3602 3701: 100 bp 40456: contig of 3362 bp 57 40556: gap of 100 hr 77 44872: con+1-4 13173: gap of 4 15155: cont. 6 15255: gap of 17626: cont. 9659: contig of 1691 bp in 29983: gap of 100 bp 33054: contig of 3071 33154: gap of 100 bp 36994: contig of 3840 23898: contig of 2210 bp in length 23998: gap of 100 bp 26021: contig of 2023 bp in length 44972: gap of 100 bp 49433: contig of 4461 bp 11704: 27620: 26121: 91251: 73256: gap of 68361: gap of 86599: 29883: rr 27520: cont 91151: cont 251: gap 98153: c 11604: contig of 1845 bp in length 704: gap of 100 bp 13073: contig of 1369 bp in length 73156: contig of 4795 k 79722: 5049: 3601: gap of contig of 6677 b p of 100 bp contig of 2263 k p of 100 bp contig of 4476 bp in length p of 100 bp contig of 1399 l of 100 bp contig of 1545 bp in length of 100 bp contig of 1348 bp in length contig of 4552 bp in contig of contig of 1074 bp in length contig of 1354 bp in contig of 100 100 bp f 6466 k 100 bp 100 bp 100 bp bp in length þþ đđ þþ ďα ďα bp in length ďα dq bp in bp in length bp in length bp in length ni dq 'n 'n in length 'n in length in length length length length length length length length

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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137994: gap of 100 bp
149790: contig of 11796 bp in length
149890: gap of 100 bp
175625: contig of 25735 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116918: gap of 100 bp
127763: contig of 10845 b
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110113: cont
                                                                                                                                          .36994
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1: contig of 4969 bp
2: contig of 5791 bp
3: contig of 5791 bp
   0;
 Score 19.8; DB 2;
Pred. No. 5.3e+02;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 bp
25735 bp in length
                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bp in
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                              Length 175625;
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Gaps
0;
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MEDLINE
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AE004513/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-MAY-2000) Department of Medicine and University of Washington Genome Center, University Box 352145, Seattle, WA 98195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 15470)

2 (bases 1 to 15470)

Stover.C.K., Pham,X.-Q.T., Erwin,A.L., Mizoguchi,S.D., Warrener,P., Hickey,M.J., Brinkman,F.S.L., Hufnagle,W.O., Kowalik,D.J., Lagrou,M., Garber,R.L., Goltry,L., Tolentino,E., Westbrook-Wadman,S., Yuan,Y., Brody,L.L., Coulter,S.N., Folger,K.R., Kas,A., Larbig,K., Lim,R.M., Smith,K.A., Spencer,D.H., Wong,G.K.-S., Wu,Z., Paulsen,I.T., Reizer,J., Saier,M.H.,
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Nature 406 (6799), 959-964 (2000)
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Pseudomonas aeruginosa PA01, section
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa
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/protein_id="AAG04170.1"
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complement(999.
/gene="PA0781"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MFDTRLIRLPDQSHTHAHEHHQLVMSLAGRAEFEVNGCGGEVCR
MRACLVPGEAGHVFAGVGDNRMLIIDLGEDNPTPEDPDLLARLFEAPRYPTLDADFQN
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DDVRLKMQQDRYAFASEIRDLEGPFTSLKLDAAYTKYEHKEIEDGETGTTFKNEGYEG
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/transl_table=11
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/codon_start=1
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126. .878
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DALYDTVIEKYRRAVRIYAPVGAHKDLLEYLVERLLENGANSSFVHKLVDPRVPVETL
IQHEVTQLAGKKILANDRIPLPQAIFGAGKKNSOGIIMNIQONGWRELELAYKHLTRQ
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TSLIAARTVELMFEAGLPKDVIALLEGGGFCRDARVAGVAGTAFTGSTDTARIIN
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STDGYTTLGASLGYNFDLGESRWLAFVKGTNLINQTVRYASSILRDRVPAAGRGIEAG
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SFGARLEHTRVDPDAKGNERFAENDGSQSFTTGSLSTGAVYKLTPIWSLAATLSYTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTMGVHSRNEETARRIEELARVGNLYINRNQIGAVVGVQPFGGHGLSGTGPKAGGPNY
LLRFVSERTTSVNTTAVGGNASLLSLADAE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RQLAEKPGAIATLIAETGGQNAMIVDSTALPEQVIKDAVQSAFTSAGQRCSALRVMYV
QQDIAERVIELLKGAMAELKVGPTEVRVSDVGPVIDAEAKAGLEQHIAALKAAGKLIA
ETKYPGNLNGHFVAPVAFEISGIDELKKENFGFVLHVVRYAAQDLEKVVQAINATGEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRCLPVLVWLTLLGRELGARIPLRLVKGAYWDSEIKQCQVQGADGYPVYTRKEGTDTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTAADAEKYMADYRQAIDTVGAEPQVGPGPRPSISIKLSALHPRYEVAQRERVLSEL
FANVLELAVRARKLNVGITIDAEEADRLELSLELYEKLMRDPAIAGWGEFGLVIQAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRLVQRSGEPVIRAAMNQAMKLMGKQFVLGRTISEALKNGRPCREQGYTYSFDMLGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAATADALIRDKLSAADWQRHLGQSDNVLVNFAAWGLVMTGKVVNIDERTDGRAPSVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGPDGIEAIRRNARALIETVRSRDNAVDTLDALLRQYSLDTQEGLMLMCLAEALLRVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="proline dehydrogenase PutA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="putA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YIGLLASGRHRNEEGEVVAAGDDEALPEYLYSGVRADFYGVEAQDRIHLLESPYGNFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APTFYELYANGPHAATGTYEVGDADADKEKAVSTDLALRFDNGVHKGSVGVFYSRFSN
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9741. .10379
                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(8685. .9614)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IELKDATSFDMLKGASFIGVISLMAWGLGYFGQPHILARFMAADSVKSIPAARRISMT
WMILCLGGAVAVGFFGIAYFQAHPEQAGAVSENPERVFIELAKILFNPWIAGVLLSAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation="MFKASHVLQGEDQTRSAAEFFPVISANYAVDEEAYLGELLQLAD/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (8685. .9614)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt TGLYEIIPGFLFASVAIVVFSLLGKAPSTSMLKRFDDAEQEYREAHQGSAAPVTQR"}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="putP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="PA0783"
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                                                                           .10379
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gene

CDS

CDS gene

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gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPVLGADGADLAAALQTIREIGDAAALDEAVDDAFFGSRLHIDNPGGRFEVLIEOPGL
LRPLRTAELSDGTLRYLLWIAALLSPRPPALLVLNEPETSLHPDLLPALGRLVGQAAQ
HSQVLVVSHAARLVATLEEHPECHSLGLEKDEGETRIQGLRELDRPAWYWEVR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVPLPAVTEAFVAAAFHPOPEORSLAMOADLALSDOLVGELFDSDLLVISTPMYNFSV
PSGLKAMIDOIVRLGVTFDFVLDNGVAQYRPLLRGKRALIVTSRGGHGFGPGGENQAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="probable acyl carrier protein phosphodiesterase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
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FDINEGSKLELGSTAKLRVLASYLETVAQIHRDYGGMSVAELRKVEVEPLDFILAWGI
DYLVASRDRDLSAMLQAAMERRYSASPYESFFTGGGLHTFNNFRKEDNGRRPMLLEAL
                                                                                                                                                                                                                                                     NFAARQDIVLTYLNSVPLSAAPGYGEVTGLADGLWWWYGADYRQVGEALDGKAGLAAQ
GLALRQVLALMIAHRRPSFYLAPRGRDELDRWTDSHLRVLTQAGVIEAPLRDAALAQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="PA0787"
10750. .11913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="PA0786"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10389.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NHADPWLRTALGFIGIDEVTVVAAEGEESGGRSFEDSCDEAEQRLLALARSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MSRILAVHASPRGERSQSRRLAEVFLAAYREAHPQARVARREVG/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="GI:9946675"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="PA0787"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MAWFHLLVAAAFEVAFAMGMKFSNGFGRLWPSLLTVVAAIGGIY/
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                                                               WVKYRDKDANQRLETFLDGLRPWPVRLAAIHRYLQPQADLASFSAFLRERLPRGSLTD
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В
AE008794
          RESULT 15
                                                                                                     Matches
                                                  3826 CACGCAACAGCGCCTCGGCCAGACAC 3801
                                                                1 cacgcaaaggcgcgtcggccagccac 26
                                                                                                    Conservative
                                                                                                       0;
                                                                                                        Mismatches
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Query Match

Local

Similarity

67.6%; 84.6%;

Score 19.6; DB 1; Pred. No. 1e+03;

Length 15470; Indels

0;

0;

4

CDS gene

FEATURES SOUTCE Gene CDS	COMMENT	JOURNAL PUBMED REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE	SOURCE ORGANISM	ACCESSION VERSION	LOCUS DEFINITION
Coding sequences below are predicted from manually evaluated Computer analysis, using similarity information and the programs; GLIMMER; http://www.tipi.org/softlab/glimmer/glimmer.html and GeneMark; http://wpal.biology.gatech.edu/GeneMark; EC numbers were kindly provided by Junko Yabuzaki and the Kyoto and Pedro Romero and peter Karp at EcoCyc. The analyses of ribosome binding sites and promoter binding sites were kindly provided by Heladia Salgado, Julio Collado-vides and RequonDB; http://kinich.cifn.unam.mx:8850/db/regulondb_intro.frameset This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistries or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence Location/Qualifiers Jorganism="Salmonella typhimurium LT2" Strain="MZC" Jorganism="Salmonella typhimurium LT2" Jorgane="MZC" Jorganism="Salmonella typhimurium LT2" Jorgane="MZC" Jorde="MZC" Jorde="MZC	Park Bouleward, St. Louis, MO 63108, USA Supported by NIH grant 5U 01 AI43283	Nature 413 (6858), 852-856 (2001) 11677609 2 (bases 1 to 26591) The Salmonella typhimurium Genome Sequencing Project. Direct Submission Submitted (29-MAR-2001) Genome Sequencing Center, Department of Genetics, Washington University School of Medicine, 4444 Forest	1 (bases 1 to 26591) MCCleilland,M., Sanderson,K.E., Spieth,J., Clifton,S.W., Latreille,P., Courtney,L., Porwollik,S., Ali,J., Dante,M., Du,F., Hou,S., Layman,D., Leonard,S., Nguyen,C., Scott,K., Holmes,A., Grewal,N., Mulvaney,E., Ryan,E., Sun,H., Florea,L., Miller,W., Stoneking,T., Nhan,M., Waterston,R. and Wilson,R.K. Complete genome sequence of Salmonella enterica serovar Typhimurium LT2	Salmonella typhimurium LT2. Salmonella typhimurium LT2 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Salmonella	3006468 GI:16420649	AE008794 26591 bp DNA linear BCT 25-OCT-2001 Salmonella typhimurium LT2, section 102 of 224 of the complete

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-10_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                35_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /Protein_id="AAL21022.1"
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4493. .6073
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/note="Ortholog of E. coli putative transport protein
(AAC/5124.1); Blastp hit to AAC/5124.1 (549 aa), 90%
identity in aa 23 - 549"
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4476. .6073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(2224. .2673)

/gene-"wzb"

/EC_number-"3.1.3.48"

/notc="Ortholog of E. coli probable
protein-tyrosine-phosphatase (AAC75122.1); Blastp hit to
AAC75122.1 (147 aa), 83% identity in aa 1 - 146"
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GIESPQALEEHGISVYASIPLSEWQKARDSVKTIKGIKRYKQSQLLAVGNPTDLAIE
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acid export"
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DQNOIQVKGVILNSIFRRATGYQDYGYYEYEYQSDSK"
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Search completed: July 31, 2002, 14:00:49 Job time: 17491 sec
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Matches 22
                                                                                                                      ch 67.6%;
l Similarity 84.6%;
22; Conservative
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76% identity in aa 1 - 617"
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/note="putative RBS for asmA; RegulonDB:STMS1H002265"
complement(8054. .8649)
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                                                                                                                                                                                                                                          Score 19.6; DB pred. No. 9e+02;
                                                                                                                                                                                                                                                                     DB 1;
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Minimum DB seq length: 0
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137.8
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556.4
552.2
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    No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1 US-08-941-445A-4

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Sequence 4, Application US/08941445A
Patent No. 6107060
GENERAL INFORMATION:
APPLICANT: Keeling, Peter
APPLICANT: Guan, Hanping
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,445A
FILING DATE: 30-SEP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/026,855
FILING DATE: 30-SEP-1996
AFTORNEY,AGENT INFORMATION:
NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 89-97
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4800 base pairs
                                                                                     ORGANISM: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle
                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                              MOLECULE TYPE: DI
    NAME/KEY:
LOCATION:
LOCATION:
LOCATION:
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CITY: Boulder
STATE: CO
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COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: doub
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..2144, 2226..2289, 2413..2513, 2651..2760, 2858
..3101, 3212..3394, 3490..3681, 3793..3879, 3977
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                                                                                        CORRESPONDENCE ADDRESS: and Sullivan,
                                                                                                                               APPLICANT: Keeling, Peter
APPLICANT: Guan, Hanping
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
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STREET: 5370 MGCITY: Boulder STATE: CO COUNTRY: US ZIP: 80303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGCGTCTTCTTCGTGCTCTTGCCGCGTGCATGATGCATGTTTTCCTCCTGGCTTGTGTT 1648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCGCGCGCGGGGGCAGGTTCCCGTCGCTCGTCGTGTGCGCCAGCGCCGGCATGAACGT
                                                                                                                                                                                                                                                                                                                                                                                                                    CTCTGATGCCTGCAACTGCAAATGCATGCAGATCAAGATGGGAGACGGGTACGAGACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGGCCACCGAGACCAGATTCAGATCACAGTCACACACCCGTCATATGAACCTTTCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tatatccgccacatgaattatcacaattcacatgctcctgcacatttctgcaagacttta 3686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGTGTATGTGACGTGTTTGCTTCGGGCATGCATGCAGGCGAACGGGCACCGTGTCATGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ct-----gactggctggatctcgcagatcaaggtcgttgacaggtacgagagggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCTCTCCCCGCTACGACCAGTACAAGGACGCCTGGGACACCAGCGTCGTGTCCGAGGTA
                                                                            5370 Manhattan Circle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59;
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US-08-679-645-25

Sequence 25, Application US/08679645 Patent No. 6350934

GENERAL INFORMATION:

APPLICANT:

Zwick, Michael G. Edington, Brent E. McSwiggen, James A.

APPLICANT:
APPLICANT:

Merlo,

Patricia Ann

Owens

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (303) 499-8089 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                           3196 cgacagat------tccggcgtccaggttttcagggcctgaggccccggaa 3240
                                                                                                                                                                                                                                                                                                                                                                          3136 cgccatggcggctctggtcacgtcccagctcgccacctccggcaccgtcctcagcgtcac 3195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                    3415 tggcggcctcggcgacgtcctcggggggcctccccgccgccatggccg
                                                                                                                                                              3295 gcaaagcaggaaaccgcaccgattcgaccggcggtgcctctccatggtggtggtgcgccac 3354
                                                                                                                                                                                                                                            3241 cccggcg-----gatgcggcgctcggcatgaggactgtcgggagcgagcgccgccccaaa 3294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CI
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 30-SEP-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                       3355 gggcagcggcatgaacctcgtgttcgtcggcgccgagatggcgccctggagcaagac 3414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                  569
                                                                                                                                                                                                                                                                                        509
                                                                                                                                                                                                                                                                                                                                                         449 CACCATGTCGGCTCTCACCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGC 508
746 CGGCGGCCTCGGTGACGTCCTCGGTGGCCTCCCCCCTGCCATGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Winner, Ellen P
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                     ---CGGCGCCGGCATGAACGTCGTGTTCGTCGGCCGAGATGGCCCCCTGGAGCAAGAC
                                                                                                                                         GCAGCAGCGGTCGGTGCCAGCCTGGCAGCCCGAGGTTCCCCTCCGTCGTCGTGTACGCCAC 688
                                                                                                                                                                                                                                                                                                                                                                                                                                241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
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not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                82;
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US-08-679-645-25
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Matches 221; Conserv
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TITLE OF INVENTION: M
TITLE OF INVENTION: I
NUMBER OF SEQUENCES:
3196 cga-----cagattccggcgtccaggttttcagggcctgaggccccggaacccggcgga 3249
                                                                                                                                                                                                                                                                                          3136 cgccatggcggctctggtcacgtcccagctcgccacctccggcaccgtcctcagcgtcac 3195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/6
FILING DATE: JULY 12, 1996
                                                                                                 3304 gaaaccgcaccgattcgaccggcggtgcctctccatggtggtgcgcgccacgggcagcgg 3363
                                                                                                                                                       3250 tgcgg-----cgctcggcatgaggactgtcggagcgagcgcccccaaagcaaagcag 3303
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LENGTH: 2267 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: September 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 6
FILING DATE: July 13,
APPLICATION NUMBER: 0
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ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                     STATE: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (213) 955-0440
TELEX: 67-3510
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                                                                                                                                    GCAGCAGCAGCGCGCGCGCGGGGCCAGGTTCCCGTCGTCGTCGTGTGCGCCAGCGC
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                                                                                                                                                                                                                                                                                                                                               Conservative
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Young, Scott A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Merlo, Donald J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Folkerts, Otto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYSTEM: IBM P.C. DOS 5.0
Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPOSITION AND METHODS FOR MODULATION OF GENE EXPRESSION IN PLANTS
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                                                                                                                                                                                                                                                                                                                                      Score 118.8; DB 4;
Pred. No. 1.2e-18;
""smatches 117;
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; TOPOLOGY: linear
; MOLECULE TYPE: DNA (gen
US-08-470-720-2
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                                                                                                                                                                                                                                                                                                        Query Match 2.2%;
Best Local Similarity 57.8%;
Matches 247; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703) 836-20 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                 3539 gcaggccaacggtcaccgggtcattggtcatctccccgcgctacgaccagtacaaggacgc 3598
                                                                                                                                                                                        3425
                                                                                                                                                                                                                                                3365 ggcatgaacctcgtgttcgtcggcgccgagatggcgccctggagcaagactggcgcgctc 3424
                                                                                                         3484 tataaatgtttcttcctgcagccatgcctgccgttacaacgggtgccgtgtc----cgt 3538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 2549 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 09-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US 08/070,455
                                                                                                                                                       172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: GENETICALLY ENGINEERED MODIFICATION OF TITLE OF INVENTION: POTATO TO FORM AMYLOPECTIN-TYPE STARCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                          112 GGAATGAACTTGATCTTTGTGGGTACTGAGGTTGGTCCTTGGAGCAAAACTGGTGGACTA 171
292 TTAGGCCCGCGGACATCGGGTAATGACAATATCCCCCCGGTTATGACCAATACAAAGATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             473 CGGCGACGTCCTCGGCGGCCTGCCGGCCGTGGCCGCGAATGGGCACC 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Alexandria
STATE: Virginia
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/470,720
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                                                                                                                                                 9909ac9tcctc999999cctcccc9cc9ccatggcc9taag-cttgcgccactgccttct 3483
                                                                       CCTACTCATTCATTACTTATTTTGTTTAGTTAGTTTCTACTGCATCAGTCTTTTTATCAT
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SYSTEM: PC-DOS/MS-DOS
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703) 836-2021
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                                                                                                                                                                                                                                                                                                                        Score 83; DB 1;
Pred. No. 3.9e-10;
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                                                                                         Query Match
Best Local (
                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                           TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
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1437
                                   3365
                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/070,455 FILING DATE: 09-JUN-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: GENETICALLY ENGINEERED MODIFICATION OF TITLE OF INVENTION: POTATO TO FORM AMYLOPECTIN-TYPE STARCH
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                              NAME: Crane-Feury, Sharon REGISTRATION NUMBER: 36,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/470,720
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                 ggcatgaacctcgtgttcgtcggcgccgagatggcgccctggagcaagactggcgcctc 3424
GGAATGAACTTGATCTTTGTGGGTACTGAGGTTGGTCCTTGGAGCAAAACTGGTGGACTA 1496
                                                                                       Similarity
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PERSSON, Per T
WIKSTROM, Olle
TAILBERG, Annell
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                                                                       Conservative
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                                                                                         2.2%; 57.8%;
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                                                                                         Score 83; DB 1;
Pred. No. 5.3e-10;
                                                                         Mismatches 165; Indels
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                                                                                                    TELEFAX: (619) 235-01 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                                                   REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
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TOPOLOGY: 1
MOLECULE TYPE:
                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                  LENGTH: 19124 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                            FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
                                  STRANDEDNESS:
                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                           NAME:
                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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620 Newport Center Drive 16th
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Wellems, Thomas E.
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Miller, Louis H.
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                  linear
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AND PLASMODIUM FALCIPARUM ERVTHROCYTE BINDING PROTEINS
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HYPOTHETICAL: ANTI-SENSE:

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                                Sequence 14, Application US/08232463 Patent No. 5670367
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Best Local :
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                      GENERAL INFORMATION:
                                                                                             15529 AAAAAATTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAT
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  APPLICANT:
           APPLICANT:
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                                                                                                                789 gcaaactttatcattatttgtctaaattaattttttct 826
                                                                                                                                                                                                                                                                           Local
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SCHEIFLINGER,
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1435
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IMMEDIATE SOURCE:
CLONE: pTZgpt-F1s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELLEFAX: (,, grant of the second of the sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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CITY: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watch 1.7%; Score 64.8; DB 1
Local Similarity 4.5%; Pred. No. 1.3e-05;
nes 18; Conservative 232; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                     gcacgcaaaggcgcgtcggccagccacgacgccgctggaaagcgcgccggcgaaccgaga 1794
                                                                                                                                                                                                                                      ggcgagagcgagagcacacatggcccccagaactgaaagcgagggagcacacgagaaggc 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ctgcagaggaagcaatcccgggccatgcagcgccattgccacgccccagcgaaaagcgaa 1554
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US-08-232-463-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
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1244 THE TATE TATE THE TATE TAREFULL TA
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NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
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                                                                                                                                                                                                                                  442 tttatgcctcatttggaaatttcgttttgaaaattatgctagtacacacttattcttgta 501
                                                                                                                                                                                                                                                                                                                                                                                                  382 ttcttcattttttatttttattttattttcttcttctttaagggtaataccaatgatactaa 441
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                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 4.8%; Pre 
nes 19; Conservative 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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1800 Diagonal Road, Suite 500
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IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.6%; Score 62.2; DB 1; Length 7218;
4.8%; Pred. No. 5.3e-05;
Live 225; Mismatches 153; Indels 0
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US-07-867-106-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/07867106 Patent No. 5389526
                                                      Matches 214; Conservative
                                                                  Query Match 1.6%; Score 58.8; DB 1; Length 5852; Best Local Similarity 49.1%; Pred. No. 0.0003;
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                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 215-568-3439 INFORMATION FOR SEQ ID NO: 2:
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APPLICANT: Williams, Keith L
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                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: RITELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Improved Plasmid Vectors for Cellular TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
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                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
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                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
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                                                                                                                                                                    PRIOR APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
                                                                                                                                   APPLICATION NUMBER: CH 0016/97 FILING DATE: 31-DEC-1996
                                                                                                                                                                                                      APPLICATION NUMBER: US/08/998,416 FILING DATE: 24-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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Knechtle, Philipp
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Steiner, Sabine
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US-07-867-106-2/c
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                                                                                                                                                              APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 538952
STREET: One Liberty Place 46th Floor
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/867,10
                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                        APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith
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ORIGINAL SOURCE:
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LENGTH: 658 base pairs
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                                                                                                                          COUNTRY:
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                                    Version #1.25
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PRIOR APPLICATION DATA:

FILING DATE:

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                                                                                US-08-947-823-1
                              Sequence 1, Application Patent No. 6114605
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 228; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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APPLICATION NUMBER: PCT/AU90/0
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5429
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LENGTH: 5852 base pairs
                                                                                                                                            5369
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 APPLICANT:
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LOCATION:
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                                                                                                                                                                                                                                                                                              CCAGGCAAAATAAACAGCATCAGAAATCTCATTAAATGTTGGTCTCAAAAAGTTTTATTAA
                                                                                                                                                                                                                                          aagggaaataccaatgccactaatccattccatcttagaaaatctctttatcttaccaaaa
                                                                                                                                                                                                                                                                                                                                          ATTTTTTAATTAATAGTACTGCACGGATTAATATGGAAATGGATACTAGATCCTTTTTC
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                                                             Application US/08947823
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Williamson,
Kaloshian,
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UMBER: 35,134
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 Isgouhi
                  Valerie M.
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Pred. No. 0.0011;
0; Mismatches 236;
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Best Local Similarity
Matches 238; Conserv
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APPLICANT:
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TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Pest Resistance in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 6 FILING DATE: 10-OCT-1996 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                           185 acctaagaggaaattcagttttatactagttttcagttttattattgtttattaagtgttt 244
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OPERATING SYSTEM: PC-DOS/MS-DOS
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AACCCCTACCAAGATTATTAGGCTATTATTTTTTATTCTATAGTAAAAAACAAATGATGAA 13319
                                                                                       AAACTTTAAGATATCTTTTGATATTTGTTCAATAATAAATTCAACTTCTTTATCTTATGA 13259
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Pred. No. 0.005;
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US-08-998-416-186
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   Query Match
Best Local Similarity
Matches 217; Conserv
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                                                                                                                                                                                                                                                       TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY_AGENT IMPORMATION:
NAME: Mel9s, J Timothy
REGISTRATION NUMBER: 38,241
REFERENCE_DOCKET NUMBER: PF/5-30306/A/CGC1976
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APPLICANT:
                                                                                                                           MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 615 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
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TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
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                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                              ORGANISM:
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Research Triangle Park
No. 6239264th Carolina
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   1.48;
ilarity 46.18;
Conservative
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Knechtle, Philipp
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Steiner, Sabine
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     0,
Score 54.2; DB 4;
Pred. No. 0.0013;
0; Mismatches 253;
                                 DB 4; Length 615;
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Gaps
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US-08-998-416-1137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 001
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,24
                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                           CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                       STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina
                  REFERENCE/DOCKET NUMBER:
                                                                                                                                            CLASSIFICATION:
                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 24-DEC
                                                                                                                                                                                                            SOFTWARE:
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Steiner, Sabine
Mohr, Christine
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IBM PC compatible
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No. 6239264artis Corporation
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N: 435
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                               38,241
             PF/5-30306/A/CGC1976
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Best Local 9
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                                                                                                                                                                 GENERAL INFORMATION:
                                                      APPLICANT:
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ORIGINAL SOURCE:
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APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
                                                                                          APPLICANT:
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                                                    Wendland, Jurgen
Knechtle, Philipp
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Pohlmann, Rainer
Steiner, Sabine
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                                                                                          Mohr, Christine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
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LENGTH: 837 base pairs
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TELECOMMUNICATION INFORMATION:
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607 ttagaaaactttagtattttgattgtgttttagtttttatttcattttgtttcttcttta 666
                                     316 agtattatacacccatttttgcagtcataaaattatgcaatttcagtacaaattgtgcgc 375
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: UZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 3054 Cornwallis Road CITY: Research Triangle Park
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Result	Score	Query Match	% Query Match Length	DB	ID	Description
1	325.8	8.6	527	9	AW448831	AW448831 BRY 1580
N	293.4	7.8	579	10	BE402419	9 CSB
ω	293.2	7.7	558	10	BE602243	BE602243 HVSMEh009
4	291.6	7.7	638	ø	AL508959	AL508959 AL508959
υī	283.8	7.5	639	10	BE414303	BE414303 SCU008 CO
6	278.8	7.4	700	9	AL508163	AL508163 AL508163
7	258.8	6.8	513	9	AL508933	AL508933 AL508933
8	248	6.6	677	10	BE414500	BE414500 SCU010.D1
. 6	247	6.5	700	9	AL506567	AL506567 AL506567
10	231.4	6.1	444	10	BM368238	BM368238 EBed01_SQ
11	220.6	5.8	494	9	AW448811	AW448811 BRY_1487
12	210.2	5.6	462	9	AL506396	AL506396 AL506396
13	178.4	4.7	375	9	AW448845	AW448845 BRY_1622
c 14	118.6	ω 1	1885	10	BE420745	BE420745 HWM002.B0
c 15	114	3.0	1135	12	CNS033GQ	AL226115 Tetraodon
16	112	3.0	879	12	CNS01JRG	
17	111.8	3.0	470	10	C73133	C73133 C73133 Rice

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44	41 42 43	38 39 40	35 36 37	ωω	30	28	25 26 27	22 23 24	18 19 20 21
101.2 101	101.8 101.6 101.6	102.4 102.2 102	102.8 102.8 102.6	103.6	104	104.4	105.8 105.4 104.6	109.4 106.4 106.2	111.4 110.4 110.2 109.4
2.7	2.7	2.7	22.7	2.7	2.7				2.9
865 855	1309 622 966	924 1185 656	848 870 1139 1223	614 960	834 1184	1101	1317 964 1101	1198 1101	1036 1059 907 855
12 12	10 12 10	10 10	3 12 12	NN	12	12	10 10	12	12 12 12
AQ324474 AZ183849	BE420736 CNS04RQH BM415686	BM415947 BF273407 CNS01ZJA	BI644518 AQ330286 AQ897537 B12981	CNS0152H AG031602	B12387 B13117	CNSOOKB5	BE420688 BM416130 CNS0153V	BM415641 B08337 CNS012JN	CNS03LWJ CNS00Z2B CNS021J4 B1645015
		BM415947 OP21029 M BF273407 GA_Eb001 AL174367 Tetraodon	Bi644518 OP2257 Mi AQ330286 nbxb0046J AQ897537 HS_3153_A R12981 T24D11-Sp6	AL104915 Drosophil AG031602 Pan trogl	B12387 F21E20-Sp6. B13117 T9K3-Sp6.2				AL250012 Tetraodon AL097133 Drosophil AL176953 Tetraodon Bi645015 Op2815 Mi

ALIGNMENTS

RESULT 1

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                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Appels R
Div. of Plant Industry, CSIRO
Canberra ACT 2601 AUSTRALIA
Tel: 61 62 465496
Fax: 61 62 465000
                                                                                                                                                                                                                                                                                                                                                         Email: rudi@pi.csiro.au
International Triticeae EST Cooperative
http://wheat.pw.usda.gov/genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anderson.O.A., Appels.R., Bailey.P., Blake.T., Close.T., Cloutier, S., Dubcovsky.J., Feuillet.C., Gale.M., Graner,A., Gustafson.P., Holton.T., Jacquemin.J.M., Jia.J., Joudrier.P., Hermann, R.G., Holton.T., Jacquemin.J.M., Jia.J., Joudrier.P., Langridge,P., Lazo.G.R., Lin.J.J., McGuire.P., Ogihara.Y., Pecchloni,N., Qualset.C., Schuch.W., Selvaraj.G., Shariflou,M., Sorrells,M., Warburton,M. and Wenzel.G.
International Triticae EST Cooperative (ITE:): Production of
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(bases 1 to 579)
    109
/note="Vector: Lambda Zap/Bluescript; Site_1: XhoI; Site_2: EcoRI; Plants grown in Phytotron with 18C/13C (day/night) 16 hour light. M13 Reverse sequencing prin used. 1.0 Kbp average insert size."

207 c 189 g 72 t 2 others
                                                                                                                    /tissue_type="endosperm"
/dev_stage="8-12 days post anthesis"
/lab_host="Escherichia coli SOLR"
                                                                                                                                                                                                               /db_xref="taxon:4565"
/clone="CSB007G05"
                                                                                                                                                                                         /clone_lib="ITEC CSB Wheat Endosperm Library"
                                                                                                                                                                                                                                                                /cultivar="Wyuna"
                                                                                                                                                                                                                                                                                    organism="Triticum aestivum"/
                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Best Local Similarity
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                                                                                                                                                                                                                   100 Jordan Hall, (Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE602243

558 bp mRNA linear EST 22-OCT-2001
HVSMEh0098D06f Hordeum vulgare 5-45 DAP spike EST library
HVCNAA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0098D06f,
                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 558)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D.,
Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fento,R.D., Close,S.J., Oates,R. and Main,D.
                                                                                                                                                                                  Email: rwing@clemson.edu
Total hg bases = 215
                                                                                                                                                                                                                                                                                                                                                                   Development of a genetically and physically anchored EST for barley genomics: Morex 5-45 DAP spike cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST
                                                                                                                                                               Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                                            Clemson University
                                                                                                                                                                                                                                                                                                Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                  On Aug 21, 2000 this sequence version replaced gi:9859804
                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hordeum vulgare
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                                                                                                                                                                                                                                                                                                                   Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             barley.
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                                                                                                                          quality sequence start: 16 quality sequence stop: 550.
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                 /db_xref="taxon:4513"
/clone="HVSMEh0098D06f"
                                                     /organism="Hordeum vulgare"
/cultivar="Morex"
                                                                                                         Location/Qualifiers
/clone_lib="Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.8%;
88.3%;
                                                                                                                                                                                                                                                                                                                                                       (2001)
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KEYWORDS
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HVcbNA0009 (5 to 45 DAP Spike"
/tissue_type="15-45 DAP Spike"
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                                       638 bp mRNA linear EST 04-JAN-2001
AL508959 Hordeum vulgare Barke developing caryopsis (3.-15.DAP)
AL508959 Hordeum vulgare BARKE BAL508959 HORDER CONA Clone HY10E20V 5', mRNA sequence.
          AL508959.1 GI:12035462
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pred. No. 3e-33;
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; Tritics 2 to 638, w. pleissner, K. p. and Graner, A.
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/note="vector: plasmid pBK-CMY; Site_1: ECORI; 3:-15.DAP)

/note="vector: plasmid pBK-CMY; Site_1: Garpopsis (3:-15.DAP)

/note="vector: plasmid pBK-CMY; Site_1: Garpopsis (3:-15.DAP)

/note="vector: plasmid pBK-CMY; Site_1: Garpopsis (3:-16.DAP)

/note="vector: plasmid partery of cDNA) and XhoI

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/db_xref="taxon:4513"
/clone="HY10E20V"
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s; pred. No. 5e-33;
s; 0; Mismatches
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RESULT 6
                                                                   3389 gccgagatggcgccctggagcaagactggcggcctcggcgacg 3431
                                                       597 GCGGAGATGGCGCCCTGGAGCAAGACCGGCGGCCTCGGCGACG 639
                                                                                             3329 tgcctctccatggtggtgcgcgccacgggcagcggcggcatgaacctcgtgttcgtcggc 3388
                                                                                 537 TGCCTCTCCATGGTGGTGCGCGCCACGGGCAGCGGCATGAACCTCGTGTTCGTCGCGGC 596
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                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
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Best Local Similarity 7.5
Matches 313; Conservative
                                                                                                                                                                            3212 ccaggttttcagggcctgaggccccggaacccggcggatgcggcgctggcatgaggact 3271
                                                                                                                                                                 3152 gtcacgtcccagctcgccacctccggcaccgtcctcagcgtcaccgacagattccggcgt 3211
                                                                                                                                                                                                         357 GTCACGTCGCAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTTCCGGCGT 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Centre for Plant Conservation Genetics, Southern Cross University Tel: 61 2 6620 3409
Emax: 61 2 6620 2409
Emaxl: tholtonescu.edu.au
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                         /organism="Triticum aestivum"
/oLone_regrentaton:4565"
/clone_rib="TpEC SCU Wheat Endosperm Library"
/tissue_type="endosperm"
/note="Vector: Bluescript II SK(-)"
86 t 12 others
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SCU008.CO4.R990714 ITEC 639 bp mRNA linear EST 24-JUL-2000
BE414303 Clone SCU008.CO4, mRNA sequence.
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9.48, 89.58; 11ve 9cgc, 11 11 3TGCGCG 11 11 11 11 11 11 11 11 11	word your vidgare yota, Viridiplants atophyta; Magonatic seek, W. Tordeum. seek, W. Tordeum. seek, W. Tordeum. seek, W. Weschke, W. quencing and analy its for Plant Gene michalekejpk gater istr 3, D-06466 Gar mer: 73 primer for 1. 700 Plant Gene michalekejpk gater Location/Oualifi /Ouganism="hordeu /Ouganism="hordeu /Ouganism="hordeu /Ouganism="hordeu /Ouganism="hordeu /Oualifi /Outhivar="barke" /Oualifi /Outhivar="barke" /Clone="HO7010y" /Clone="HO7010y" /Issue_type="deve" /Issue_type="deve" /Inb. Dost="WecCor: Plaa /Fortes WecCor: Plaa /Fortes Wec	163 163 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
Seq primer: T3 primer for 5'end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Institute for Plant Genetics and Crop Plant Research Corrensstr. 3, D-06466 Gatersleben, Germany
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Hordeum vulgare cDNA clone HY10D16V 5', mRNA sequence.
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/lab_host="XLOLR"
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/clone="HY10D16V"
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/cultivar="Barke"
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GCAGGTTTTCAGGGTGTGAGGCCCCGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACT
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PO Box 157, Lismore NSW 2480 AUSTRALIA
Tel: 61 2 6620 3409
Fax: 61 2 6622 2080
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/note="Vector: Bluescript II SK(-)"

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/cultivar="Wyuna"
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Pred. No. 1.1e-26;
0; Mismatches 57;
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                                                  3163 gctcgccacctccggcaccgtcctcagcgtcaccgacagattccggcgtccaggttttca 3222
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3283 cgccgcccaaagcaaagcaggaaaccgcaccgattcgaccggcggtgcctctccatggt 3342
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                                                                                                                                                                                                                                                                                    Match 6.5%; Score 247; DB 9; Length 700; Local Similarity 89.4%; Pred. No. 1.5e-26;
                                                                                                                                                       1 GCTCGCCACCTCCGGCACCGTCCTCGGCGTCACCGACAGATTCCGGCGTCCAGGTTTTCA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hordeum vulgare
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Michalek W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST sequencing and analysis in barley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Michalek, W., Weschke, W., Pleissner, K.-P. and Graner, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
imer: T3 primer for 5'end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2: xhoI; mRNA was made from developing caryopsis (3.-15.DAP) xhoI; mRNA was made from developing caryopsis (3.-15.DAP) of spring barley variety (Barke, a high quality malting variety, Clohing sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is 1 kb sequence trimming: Vector sequences and sequence ends were trimmed from the 5'-and 3'-end until a 50 bp window
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1 229 c 218 g
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/lab_host="XLOLR"
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                        3099 cagtcgtctcttgctgcaggtagccacaccctgcgc---gcgccatggcggctctggtca 3155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R. Development of Barley Transcriptome Resources Unpublished (2001)
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Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooideae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: rwaugh@scri.sari.ac.uk
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00 44 1382 562426
                                                                                    Conservative
                                                                                                                                                                                                                                                        grains (6 days post anthesis) in glasshouse grown barley plants. Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal IGF (Investigating
                                                                                                                                                                                                                     Gene Function) project.
                                                                                                                                                                                                                                                                                                                    /note="Yector: pSPORT1; Site_1: Sal I; Site_2: Not I; Non-normalised library, directionally cloned into pSPORT1. Derived from endosperm tissue dissected from developing
                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Endosperm"
/dev_stage="6 days post anthesis"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="EBed01_SQ002_J02"
/clone_lib="IGF Barley EBed01 library"
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                                                                                                                                                                                                               3211 tccaggttttcagggcctgaggccccggaacccggcggatgcggctcggcgctcggcatgaggac 3270
                                                                                                                                                              3152 gtcacgtcccagctcgccacctccggcaccgtcctcagcgtcaccga-cagattccggcg 3210
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99tgcctctccatggtggtgcgcgccacgggcagcggcggcatgaacctcgtgttcgt-c 3385
                                                                                           TGCAGGTTTTCAGGGTGTGAGGCCCCGGAGCCCCGGCAGATGCGCCCGCTCGGCATGAGGAC 335
                                                                                                                                                GTCACGTCGCAGCTCGCCACCTCCGGCACCGTCCTCGGCATTACCGACCAGGTTCCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTTTTCAGGGCCTCAGGCCCCGGAACCCAGCGGATGCGGCGCTTTGGTATGAGGACTATCG 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gttttcagggcctgaggcccggaacccggcggatgcggcgctcggcatgaggactgtcg 3275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Bryan Clarke Division of Plant Industry C.S.I.R.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPO Box 1600, Canberra, ACT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clarke, B.C., Hobbs, M. and Appels, R. Genes active in developing wheat endosperm Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bread wheat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST
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AW448811.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW448811 494 bp
BRY_1487 BRY Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Triticeae; Triticum. (bases 1 to 494)
                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 2 6246 5054
61 2 6246 5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                            bryanc@pi.csiro.au.
                                                                                                                                                                                                                                                                                                                                                                           /organism="Triticum aestivum"
/cultivar="Wyuna"
/db_xref="taxon:4565"
/clone="p51-2A"
                                                                                                                                                                                                                                                                                                                                       /cell_type="endosperm"
170 c 160 g
                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="BRY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                       5.8%;
86.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    .494
                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                    Score 220.6; DB 9; Pred. No. 1.1e-22;
                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA clone P51-2A, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA
                                                                                                                                                                                                                                                         39;
                                                                                                                                                                                                                                                                                 Length 494;
                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                      Gaps
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179

3368 atgaacctcgtgttcgtcggcgcgagatggcgccctggagcaagactggcggcctcggc 3427

ATGAACCTCGTGTTCGTCGGCGCGCGAGATGGCGCCCTGGAGCAAGACCGGCGGCCTTGGC

CGCACCGCGGGAGCCGGCGGTGCCTCTNCGTGGTGGTNGCGCGCCACGGGCA---GCGGC 178 Gaps

<u>ب</u>

atgcggcgctcggcatgaggactgtcggagcgagcgccgccccaaagcaaagcaggaaac 3308

ATGCGGCGCTTGGTATGAGGACTATCGGAGCAAGCGCCCCCGAAGCAAAGCCGGAAAG 121

3249

62

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ORIGIN
                                                                                                                                                    BASE COUNT
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AUTHORS
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                                   Query Match
Best Local :
       Matches 251;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              396 GGTGCCTCTCCATGGTGGTGCGCGCCACGGGCAGCGCCGGCATGAACCTGTGTTTCGTCC 455
                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCGCCCAAATGGCGCCCTGGAACAAAAAACGGGG 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                michalek,W., Weschke,W., Pleissner,K.-P. and EST sequencing and analysis in barley Unpublished (2000)
Contact: Michalek W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL506396 Hordeum vulgare Barke developing caryopsis (3.-15.DAP) Hordeum vulgare cDNA clone HY02P18T 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Institute for Plant Genetics and Crop Plant Research Corrensstr. 3, D-06466 Gatersleben, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
Seq primer: T3 primer for 5'end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hordeum vulgare
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 462)
                                                                                                                                                    80
     Conservative
                                                                                                                                     contains less than two ambiguities. The maximum length was set to 700 bp" $144\ c\ 159\ g\ 72\ t\ 7 others
                                                                                                                                                                                                               note="Vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2: XhoI; mRNA was made from developing caryopsis (3.-15.DAP) of spring barley variety 'Barke', a high quality malting variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is 1 kb sequence trimming: Vector sequences and sequence ends were trimmed from the 5'-and 3'-end until a 50 bp window
                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="developing caryopsis (3.-15.DAP)"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Hordeum vulgare Barke developing caryopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="HY02P18T"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Hordeum vulgare"
/cultivar="Barke"
/db_xref="taxon:4513"
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                           5.6%;
87.8%;
  0;
Score 210.2; DB 9;
Pred. No. 3.7e-21;
0; Mismatches 31;
  Indels
                                             Length 462;
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COMMENT
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                                                          KEYWORDS
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                                                                                                ACCESSION
                                                                                                                                  DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 191; Conservative
                      ORGANISM
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                                                                                                                                                                                                                                                                                      3272 gtcggagcgagcgccgcccaaagcaaagcag 3303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 342 ACCGGAGCGAGCGCCCCCGAAGCAACAAAG 373
                                                                                                                                                                                                                                                                                                                                                                                                        222 GTCACGTCGCAGCTCGCCACCTCCGGCACCGTCCTCGGCATGACCGACAGGTTCCGGCGT 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                              GCAGGTTTTCAGGGTGTGAGGCCCCGGAGCCCGGCAGATGCGCCGCCTCGGCATGAGGACT 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW448845 375 bp mRNA linear EST 03-JAN-2
BRY_1622 BRY Triticum aestivum cDNA clone P59-1E, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Bryan Clarke
Division of Plant Industry
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                                                                                                    1885 bp mRNA linear EST 24-JUL-2001
HWM002.B02 ITEC HWM Barley Leaf Library Hordeum vulgare cDNA clone
HWM002.B02, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: bryanc@pi.csiro.au
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPO Box 1600, Canberra, ACT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bread wheat
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                                                          EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 4.7%; Score 178.4; DB 9; Similarity 90.1%; Pred. No. 1.6e-16;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                      Hordeum vulgare
                                                                            BE420745.1 GI:9418588
                                          barley.
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61 2 6246 5000
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131 c 117 g
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/db_xref="taxon:4565"
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 traatatacacataagtattatacacccatttttgcagtcataaaattatgcaatttcag 361
                                                                                                                                                                                                                                                                                                                                                 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 gtttcatgttttatttcattttctttactttttagggtaaaaccaatgcccccaattcat 181
                                    482 agtacacacttattcttgtatattatggaaaagcgcaatttctgtgtaagttttgtcatt 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 tttggtttcgctgtttttcatttcctttcttataggggtaataccaatgacagtaatt 61
                                                                                                             ggtaataccaatgatactaatttatgcctcatttggaaatttcgttttgaaaattatgct 481
                                                                                                                                                                                                                                                                                                                                                                                                                              tctacctaagaggaaattcagttttatactagtttcagttttattattgtttattaagtg 241
                                                                                                                                                          Anderson, O.A., Appeis, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y., Epechioni, N., Qualset, C., Schuch, W., Selvaraj, G., Sharifiou, M., Sorrells, M., Warburton, M. and Wenzel, G. Sorrells, M., Warburton, M. and Wenzel, G. International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Herrmann RG
Botanisches Institut der LMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: herrmann@botanik.biologie.uni-muenchen.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 49 30 171683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 International Triticeae EST Cooperative (ITEC)
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/db_xref="taxon:4513"
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/dev_stage="14 day old"
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                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                    Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Charaterization and repeat analysis of the compact genome of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Burin, H., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
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GSS; genome survey sequence.
Tetraodon nigroviridis.
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/db_xref="taxon:99883"
/clone="208p24"
/clone_lib="G"
                                                               ∕organism="Tetraodon
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Search completed: July 31, Job time: 13464 sec

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                                                                                    ctgtattttttttcatttttcttcttctggaagggtaacactaatgccactaattcatt 601
                                                                                                                                                           ggtaataccaatgatactaatttatgcctcatttggaaatttcgttttgaaaattatgct 481
                  agtacacacttattcttgtatattatggaaaagcgcaatttctgtgtaagttttgtcatt 541
                                                                tctacctaagaggaaattcagttttatactagtttcagttttattattgtttattaagtg 241
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Similarity 47.7%;
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65 c 43 g 124 t 40 others
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Pred. No. 3e-07;
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /SIDS1/gcgdata/hc
2: /SIDS1/gcgdata/hc
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ABL32411 ABL34492 ABL32717 ABL327184	ABL32859 AAS61386	AAS45300	ABL33246	AAI94064	AAQ26404 ABL32148	AAQ26401	ABL32357	AAI94068	ABL32053	ABL34022	AAS45477	AAS46336	ABL32905	ABL34358	AAI95036	ABL32972	AAS46608	AAI95044	ABL32267	AAS46774	ABL33696	ABL32098	ABL34155	ABL32527	AAS46686	ABL33697	AAS45347	9	AAS46735
	Human immune syste Human gene regulat	Tumour suppressor Chemically pretrea	Human immune syste	Human neuroblastom	Granule-bound star	SstI fr			immune	Human immune syste	Chemically pretrea	- 7	immune	immune	Human neuroblastom	Human immune syste			immune inmune	r sinne	immune	immune	immune		Tumour suppressor	Human immune syste	Chemically pretrea		Tumour suppressor

ALIGNMENTS

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misc_feature	misc_feature	repeat_region	repeat_region	repeat_region	Key repeat_region	Zea mays.	SER; starch-encapsulating glucosyl transferase; ss.	Zea mays waxy gene	11-SEP-1998 (f	AAV29752;	1 52 AV29752
<pre>/*tag= e /note= "GC stretch, potential regulatory factor binding" 442468</pre>	/"cay" direct repeat 1" /note= "direct repeat 1" 372385	02 =	/ cug- /note= "direct repeat 1" 293297 /*tag= c	N =	Location/Qualifiers 283.287 /*tag= 8		apsulating region; fusion vector; erase; ss.	ene.	(first entry)		standard; DNA; 4800 BP.

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misc_feature
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901
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2651..2760
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2055..2144
/*tag= w
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1685..1765
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/note= "transcriptional
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/note= "target duplication site (Ac7)"
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         The sequence is that of the waxy gene which codes for glucosyl transferase. It can be used in the production of a hybrid polypeptide comprising a starch-encapsulating region (SER) fused to a payload protein. The hybrid polypeptide can be used to make modified starches comprising the payload protein, selected from
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                                                                                  Hybrid polypeptide comprising starch-encapsulating region and protein - useful for, e.g. producing protein(s) resistant to degradation by stomach acids
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P-PSDB; AAW56484.
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                                                                  Example 2; Page 29-31; 156pp; English.
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  .g. hormones, growth factors, antibodies,
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3977..4105
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AC AAQ4
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DT 10-E
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DE Rice
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KW anti
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Best-Local Similarity
Matches 415; Conserv
                                        Rice starch synthase gene
                                                                           10-DEC-1993
                                                                                                                                    AAQ45913 standard;
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anti-sense;
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              Amylose; gramineae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunoglobulins, etc. The modified starch can also be used to provide grain feeds enriched in amino acids. By encapsulating the payload protein in starch, it is more resistant to degradation by stomach acids.
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                                                                                                                                                                                                                         caggttcttccactgctacaagcgcggagtggaccgcgtgttcgttgac
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                                                                        (first entry)
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                                                                                                                                    DNA; 2286
            modification; rice starch
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Pred. No. 6.2e-32;
0; Mismatches 235;
                                                                                                                                    ВP
            synthase;
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                                                                                            Query Match
Best Local
     1321
                        3196
                                                                                                                                                  Rice starch synthase gene is used to transduce rice plants when ligated into a vector. This results in the amylose content of transduced plant being modified, improving the taste of the rice
                                                                                                                                                                                                                       Plant of rice family (family gramineae) with improved amylose content - in which vector is prepd. by transducing sense or anti-sense DNA of rice starch synthase gene downstream from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
                                                                                                                                    Sequence 2286
                                                                                                                                                                                             Disclosure; Page 9-11;
                                                                                                                                                                                                                                                                   WPI; 1993-231498/29.
P-PSDB; AAR39441.
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(MITU ) MITSUBISHI KASEI CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                           intron
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                                       caccatgtcggctctcaccacgtcccagctcgccacctcggccaccggcttcggcatcgc 1320
                                                  cgccatggcggctctggtcacgtcccagctcgccacctccggcaccgtcctcagcgtcac
                       cgacagat---
                                                                                 Conservative
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/number= 1
1717..1797
/*tag= d
/number= 2
1798..1904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Stop codon not specified in specification."
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/product= rice_starch_synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1265..2197
                                                                                                                                 578 A; 508 C;
                                                                                          4.88;
                                                                                                                                                                                          17pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ٥
            -tccggcgtccaggttttcagggcctgaggccccggaa 3240
                                                                                  0,
                                                                                Score 182.2; DB 14; Length 2286; Pred. No. 1.9e-31; O; Mismatches 198; Indels 78;
                                                                                                                                480 G;
                                                                                                                                  720
                                                                                                                                 T; 0
                                                                                                                                 other;
                                                                                Gaps
                                                            3195
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AAV29753
                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1441 gcagcagcggtcggttgcagcgttggcagccggaggttcccctccgtcgtcgtgtacgccac 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3241 cccggcg-----gatgcggcgctcggcatgaggactgtcggagcgagcgccgcccaaa 3294
                                                                                                                                                                                                                      SER; starch-encapsulating region; fusion vector; starch synthase; bacterial glycogen; ss.
                                                                                                                                                                                                                                                                                                11-SEP-1998
                                                                                                                                                                                                                                                                                                                              AAV29753;
                                                                                                                                                                                                                                                                                                                                                        AAV29753 standard; DNA; 2542 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                 1978 tcgac 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                             3781 tcgac 3785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1858 atttcgcaagattttaacccaagtttttgtggtgcaattcattgcagatcaaggttgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3661 ctcctgcacatttctgcaagactttactgactggctggatctcgcagatcaaggtcgttg 3720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1738 gtgatctctcctcggtacgaccagtacaaggacgcttgggataccagcgttgtggctgag 1797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3564 gtcatctccccgcgctacgaccagtacaaggacgcctgggacaccagcgtcatctccgag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1678 ggatggatgtgtaatgttgtgttcttgtgttctttgcaggcgaatggccacagggtcatg 1737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3510 cctgccgttacaacgggtgccgt-----gtccgtgcaggccaacgggtcacgggtcatg 3563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3415 tggcggcctcggcgacgtcctcggggggcctccccgccgccgccatggccgtaagc----- 3466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1501 ---cggcgccggcatgaacgtcgtgttcgtcggcgcgagatggccccctggagcaagac 1557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3355 gggcagcggcatgaacctcgtgttcgtcggcgccgagatggcgccctggagcaagac 3414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-SEP-1997;
                             09-APR-1998
                                                                                                    polyA_site
                                                                                                                                                                                                                                                                   Oryza sativa waxy gene.
                                                         WO9814601-A1
                                                                                                                                                                                                                                                                                                                                                                                     w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gcaaagcaggaaaccgcaccgattcgaccggcggtgcctctccatggtggtgcgcgccac 3354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gtaggagcatatgcgtgatcagatcatcacaagatcgattagctttagatgatttgttac 1857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gtat-----acaattcacatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acttcgatcgctcgtcgctgaccgtcgtcgtcttcaactgttcttgatcatcgcatt 1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----ttgcgccactgccttcttataaatgtttcttcctgcagccatg 3509
                                                                                                                                                                                                                                                                                                (first entry)
97WO-US17555
                                                                                                  /product= starch (bacterial glycogen) synthase
2535
                                                                                                                                                             Location/Qualifiers
                                                                                      /*tag=
                                                                                                                                /*tag=
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PR XXX PR XXX
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XXXXXXXXX
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                                                                                                                                                                                                                                               RESULT
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified starches comprising the payload protein, selected from, e.g. hormones, growth factors, antibodies, enzymes, dyes, immunoglobulins, etc. The modified starch can also be used to provide grain feeds enriched in amino acids. By encapsulating the payload protein in starch, it is more resistant to degradation by stomach acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence is that of the waxy gene which codes for starch synthase. It can be used in the production of a hybrid polypeptide comprising a starch-encapsulating region (SER) fused to a payload protein. The hybrid polypeptide can be used to make
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hybrid polypeptide comprising starch-encapsulating region and
protein - useful for, e.g. producing protein(s) resistant to
                                                                                                                                                                                                                                                                                                                         3415 tggcggcctcggcgacgtcctcggggggcctccccgccgccatggccg 3461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3295 gcaaagcaggaaaccgcaccgattcgaccggcggtgcctctccatggtggtgcgcgccac 3354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3136 cgccatggcggctctggtcacgtcccagctcgccacctccggcaccgtcctcagcgtcac 3195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2542 BP; 610 A; 665 C; 693 G; 574 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 32-34; 156pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             degradation by stomach acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW56485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EXSE-) EXSEED GENETICS LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-SEP-1996;
                                                                                                                                                                                                            AAX60319 standard; DNA; 1915 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA sequence of the maize waxy gene
                                                                                                                                  23-AUG-1999
                                                                                                                                                                                                                                                                                                     746 cggcggcctcggtgacgtcctcggtggcctcccccctgccatggctg 792
                                                                                                                                                                                                                                                                                                                                                                              689 ---cggcgccggcatgaacgtcgtgttcgtcggcgccgagatggccccctggagcaagac 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     449 caccatgtcggctctcaccacgtcccagctcgccacctcggccaccggcttcggcatcgc 508
                                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                gggcagcggcggcatgaacctcgtgttcgtcggcgccgagatggcgccctggagcaagac 3414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cgacaggtcggcgccgtcgtcgctgctccgccacgggttccagggcctcaagccccgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cgacagat-----tccggcgtccaggttttcagggcctgaggccccggaa 3240
                                                                                                                                                                                                                                                                                                                                                                                                                                                       gcagcagcggtcggtgcagcgtggcagccggaggttcccctccgtcgtcgtgtacgccac 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Keeling P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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Pred. No. 2.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82; Indels 24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2542;
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Non-glycogen-like polysaccharide production; fermentation; waxy gene; starch synthesis enzyme; glycogen-synthesis enzyme; glycogen synthesis; non-starch branching gene; amylopectin; amylose; plant-like starch; ss.

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Best Local :
AAX63355
                        AAX63355 standard; cDNA;
                                                                                                                                       3440
                                                                                                                                                                                                                                                                                                                                                                                                                                                       3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The specification describes a method for the production of non-glycogen-like polysaccharides in a host. The method comprises transforming a host, suitable for fermentation, with genes encoding starch- or glycogen-synthesis enzymes, and fermenting the transformants. The specification also describes hosts transformed with a gene active in glycogen synthesis and at least one non-starch branching gene, involved in production of amylopectin or amylose in its original host. The method is used to produce plant-like starches by fermentation and new starches in plants. These starches are useful for all food and non-food applications of starch. The present sequence is used in
                                                                                                                                                                                                                                                                                                                              3260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1915 BP; 365 A; 610 C; 641 G; 299 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing non-glycogen-like polysaccharides in bacteria, fungi or plants - transformed with genes for enzymes involved in starch or glycogen synthesis allows fermentative production of starches with engineered properties
                                                                                                         301
                                                                                                                                                                     241
                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 49; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAY16604.
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                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                             1 atggcggctctggccacgtcgcagctcgtcgcaacgcgcgccggcctgggcgtcccggac 60
                                                         G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            course of the invention.
                                                                                                                   99cctccccgccatggccgtaagcttgcgcc 3473
                                                                                                                                                                                                                                                                                                                                                gcgtccacgttccgccgcgcgccgcgcagggcctgagggggcccggggcgtcggcggcg 120
                                                                                                                                                                                                                                                                                                                                                                              agattccggcgtccaggttttcagggcctgaggcccgggaacccggcggatgcggctc 3259
                                                                                                                                                                                                                                                                                                                                                                                                                                 atggcgctctggtcacgtcccagctcgccacctccggcaccgtcctcagcgtcaccgac
                                                                                                   ggcctgccggccatggccgcgaacgggcacc
                                                                                                                                                                             ttcgtcggcgccgagatggcgccctggagcaagactggcggcctcggcgacgtcctcggg 3439
                                                                                                                                                                                                                                            ttcgtcggcgagatggcgccgtggagcaagaccggcggcctcggcgacgtcctcggc
                                                                                                                                                                                                                         cgccgcgggggcaggttcccgtcgctcgtcgtgtgcgccagcggcatgaacgtcgtc 240
                                                                                                                                                                                                                                                                                   gcggacacgctcagcatgcggaccagcgcgcgcgcgcgcccaggcaccagcagcaggcg 180
                                                                                                                                                                                                                                                                                                                   1998-568285/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXSEED GENETICS LLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0042939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.3%;
                          2267 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 124.4; DB Pred. No. 2.8e-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 19; Length 1915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                      3196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes an enzymatic nucleic acid molecule (I) with RNA cleaving activity, which modulates the expression of a plant gene. Also described is a gene comprising a cDNA sequence encoding maize belta-9 desarturase. (I) can be used to modulate expression of a gene, preferably belta-9 desarturase or a granule bound starch synthase (GBSS) gene, in a plant (preferably a maize or canola plant). (I) can be used to modulate eaffeine synthesis in a coffee plant, nicotine production in a tobacco plant, fruit ripening processes in an apple, tomato, pear, plum or peach plant, flower pigmentation in a rose, petunia, heart and the contract of the contract
                                                                                                                                                             3304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2267 BP; 465 A; 699 C; 733 G; 370 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chrysanthemum or marigold plant or lignin production in a aspen, poplar or pine plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       synthase in maize or canola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ribozyme which modulates plant gene expression -modulates expression of DELTA-9 desaturase or graphical range = 1000 \, \mathrm{GeV}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 9; Page 31-33; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme; modulation; gene expression; transgenic plant; cleavage; canola plant caffeine synthesis; coffee plant; nicotine production; tobacco;
                 413
                                                                                                                                                                                                             293
                                                                                                                                                                                                                                                                                      173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-202224/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Edington BE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-JUL-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fruit ripening; flower pigmentation; lignin production; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Granule bound starch synthase encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-MAR-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DOWC ) DOWELANCO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
cggcatgaacgtcgtcttcgtcggcgccgagatggcgccgtggagcaagaccggcggcct
                         cggcatgaacctcgtgttcgtcggcgccgagatggcgccctggagcaagactggcggcct
                                                                                                                                      gaaaccgcaccgattcgaccggcggtgcctctccatggtggtgcgcgccacgggcagcgg
                                                                                                                                                                                                                         cggcatggcggctctagccacgtcgcagctcgtcgcaacgcgcgccggcctgggcgtccc 232
                                                                                                                                                                                                                                                                                                                                                                                                                          cyccatygcygctctyytcacytcccayctcyccacctccygcaccytcctcaycytcac 3195
                                                                                                gcagcagcagccgcgcgcggggccaggttcccgtcgctcgtgtgcgccagcgc
                                                                                                                                                                                                PAO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          corn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Skokut TA,
                                                                                                                                                                                                                                                                                                                               -cagattccggcgtccaggttttcagggcctgaggccccggaacccggcgga 3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zea mays; delta-9 desaturase; GBSS; target; substrate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Folkerts 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96WO-US11689.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.1%;
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Young SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 118.8; DB 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McSwiggen
Zwick MG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         granule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preferably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Merlo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tobacco,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         starch
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                                                     3423
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     472
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RESULT 6
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                                                                                                                                                                          cell line into which an apoptosis resistance gene has been introduced.

CC rise recombinant viruses generated are capable of expressing apoptosis.

CC associated genes. These can then be used in a variety of diseases for combinition of apoptosis by gene transfer, or where the cc inhibition of harmful apoptosis by gene transfer, or where the cancer cell are useful as vectors for gene therapy which can be applied to cancer cell selectively, the treatment of combinant viruses and graft rejection reaction, and apoptosis induction cell-therapy for inflammatory cells in inflammatory diseases. Prior arts have encountered the problem where if an adenovirus vector capable of cexpressing an apoptosis-associated gene is introduced into animal cells, the cells producing the virus will be destroyed because the period of cell improduced to induce cell death by apoptosis is shorter than that cequired to replicate and produce the virus, resulting in failure to obtain a recombinant virus having the integrated apoptosis-associated cell gene. In this invention an apoptosis resistant gene introduced) is established and overcomes the problem. The present sequence represents the base sequence of the plasmid pRx-ires-bsr, which contains the cowpox virus bsr gene, and cell is a paged in an example from the present invention.
            QΥ
                                                  Matches 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         crmA; bc1-2; bc1-x1; FLIP; survivin; IAP; IIP; adenovirus;
autoimmune disease; graft rejection reaction; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cowpox virus; bsr; viral vector; expression; apoptosis; resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX33181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX33181 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Base sequence of the plasmid pRx-ires-bsr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09913073-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cowpox virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 38-41; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hamada H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (RPRG-) RPR GENCELL ASIA PACIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-SEP-1997;
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                                                                                                                                   Sequence 6644 BP; 2166 A; 1573 C; 1424 G; 1481 T; 0 other;
2 tttggtttcgctgtttttcatttcctttcttcttaaggggtaataccaatgacagtaatt 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention describes an apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1999-243728/20
                                                                    Similarity
                                                                                                                                                                     in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97JP-0259235
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                                                                    2.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6644
                                                    0;
                                                                    Score 106.8; DB 20; Pred. No. 5.3e-14;
                                                    Mismatches 367;
                                                       Indels
                                                                                  Length
                                                                                         6644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer;
                                                       0,
                                                       Gaps
                                                         0;
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RESULT 7
AAX33182/c
ID AAX331
XX
AC AAX331
XX
DT 25-JUN
XX
COWPOX
KW CTMA;
KW CTMA;
KW autoin
XX
autoin
XX
HOMO S
XX
OS Synthe
OS Synthe
OS HOMO S
XX
OS Synthe
OS OS HOMO S
XX
XX
OS SYNTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4045
                                                                                                                                                                                                                                                                                                                                                          3805
                                                                                                                                                       Cowpox virus; bsr; viral vector; expression; apoptosis; resistance; crmA; bcl-2; bcl-x1; FLIP; survivin; IAP; ILP; adenovirus; cancer;
                                                                                                                                                                                                                                                         AAX33182 standard; DNA;
                                                                                                                                                                                                                                                                                                               3745 TTTTTTGCAACTGCAAGAGGGTTTATTGGATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122
                                                                                                                                            crmA; bcl-2; bcl-x1; FLIP; survivin; IAP; ILP; adenovirus; autoimmune disease; graft rejection reaction; inflammation;
                                                                                                                                                                                        Base sequence of the plasmid pRx-Bcl-xl-bsr.
                                                                                                                                                                                                               25-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302
                                                                            W09913073-A2
                                                                                                              Synthetic.
                                                                                                                                 inflammatory disease;
                                                       18-MAR-1999
                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                totacotaagaggaaattoagttttatactagttttoagttttattattgtttattaagtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gtttcatgttttatttcattttctttactttttagggtaaaaccaatgcccccaattcat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               catattgtgtaacagtgcgattcttgtgccaattatgtacaatttcttttgtaattgttt 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ctttaagggaaataccaatgccactaatccattc 695
                                                                                                                                                                                                                                                                                                                                                                       cttgcttagaaaactttagtattttgattgtgtttttagtttttatttcattttgtttctt 661
                                                                                                                                                                                                                                                                                                                                                                                                     ctgtatttttttcattttctttcttctggaagggtaacactaatgccactaattcatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                               agtacacacttattcttgtatattatggaaaagcgcaatttctgtgtaagttttgtcatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ttaatatacacataagtattatacacccatttttgcagtcataaaattatgcaatttcag 361
                                                                                                                                                                                                                                                                                                                                                         ggtaataccaatgatactaatttatgcctcatttggaaatttcgttttgaaaattatgct 481
                                                                                                                                                                                                              (first entry)
                                                                                                                                    SS.
                                                                                                                                                                                                                                                           7372
                                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241
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                                                                                                                                                                                                                                                                                                                                                                                                                               601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541
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08-SEP-1997;

97JP-0259235 98WO-JP04010

07-SEP-1998;

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Cell line into which an appotosis resistance gene has been introduced.

C The recombinant viruses generated are capable of expressing apoptosis. CC associated genes. These can then be used in a variety of diseases for CC which the induction of apoptosis by gene transfer, or where the induction of apoptosis by gene transfer, or where the CC inhibition of harmful apoptosis, is therapeutic. The recombinant viruses CC are useful as vectors for gene therapy which can be applied to cancer therapy for destroying cancer cells selectively, the treatment of CC therapy for inflammatory cells in inflammatory diseases. Prior arts have cencountered the problem where if an adenovirus vector capable of CC the cells producing the virus will be destroyed because the period of CC the cells producing the virus will be destroyed because the period of CC the cells produced to induce cell death by apoptosis is shorter than that CC cobtain a recombinant virus having the integrated apoptosis-associated GC gene. In this invention an apoptosis-resistant 293 cell line (having an CC apoptosis resistant gene introduced) is established and overcomes the problem. The present sequence represents the base sequence of the CC plasmid pRx-Bcl-xl-bsr, which contains the human Bcl-xl gene, and colleged in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                       4893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7372 BP; 2353 A; 1749 C; 1649 G; 1621 T; 0 other;
482 agtacacacttattcttgtatattatggaaaagcgcaatttctgtgtaagttttgtcatt 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes an apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 41-45; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 gtttcatgttttatttcattttctttactttttagggtaaaaccaatgcccccaattcat 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-243728/20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 catattgtgtaacagtgcgattcttgtgccaattatgtacaatttcttttgtaattgttt 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 tttggtttcgctgtttttcatttcctttcttcttaaggggtaataccaatgacagtaatt 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                             ttaatatacacataagtattatacacccatttttgcagtcataaaattatgcaatttcag 361
                                                                                                                                                                                                                                                                                                                           tctacctaagaggaaattcagttttatactagtttcagttttattattgtttattaagtg 241
                                                                                                         ggtaataccaatgatactaatttatgcctcatttggaaatttcgttttgaaaattatgct 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 106.8; DB 2
Pred. No. 5.6e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 20; Length 7372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Ş 밁 δÃ 밁

Sequence 7797

BP; 2542 A; 1760 C; 1656 G; 1839 T; 0 other;

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CC cell line into which an apoptosis resistance gene has been introduced.

CC the recombinant viruses generated are capable of expressing apoptosis.

CC associated genes. These can then be used in a variety of diseases for the induction of apoptosis by gene transfer, or where the induction of apoptosis by gene transfer, or where the cc are useful as vectors for gene therapy which can be applied to cancer therapy for destroying cancer cells selectively, the treatment of cc therapy for diseases and graft rejection reaction, and apoptosis induction therapy for inflammatory cells in inflammatory diseases. Prior arts have cencountered the problem where if an adenovirus vector capable of the cells producing the virus will be destroyed because the period of the cells producing the virus will be destroyed because the period of the cells producing the virus having the integrated apoptosis-associated gene. In this invention an apoptosis-resistant 293 cell line (having an apoptosis resistant gene introduced) is established and overcomes the problem. The present sequence represents the cowpox virus bar gene which cc is used in an example from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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AAX33180/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cowpox virus; bsr; viral vector; expression; apoptosis; resistance; crmA; bcl-2; bcl-x1; FLIP; survivin; IAP; ILP; adenovirus; cancer; autoimmune disease; graft rejection reaction; inflammation; inflammatory disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 34-38; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX33180 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4533
                                                                                                                                                                                                                                                                                                                                                                        The present invention describes an apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                               New apoptosis-resistant virus-sensitive cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hamada H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cowpox virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cowpox virus bsr full length gene sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX33180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4473 TTTTTTTGCAACTGCAAGAGGGTTTATTGGATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (RPRG-) RPR GENCELL ASIA PACIFIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAR-1999
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AAX33184/c
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                                                          crmA; bc1-2; bc1-x1; FIIP; survivin; IAP; ILP; adenovirus; cancer;
autoimmune disease; graft rejection reaction; inflammation;
                                                                              Cowpox virus; bsr; viral vector; expression; apoptosis;
                                                                                                  Base sequence of the plasmid pRx-Bcl 2-i-hCD
                                                                                                                        25-JUN-1999
                                                                                                                                                                AAX33184 standard; DNA; 7996 BP
                  Homo sapiens
                                                 inflammatory disease;
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                                                                                                                                                                                                                                                                                                 327;
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                                                                                                                      (first entry)
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PP (07-SEP-1998; 98WO-JP04010.

XX (RPRG-) RPR GENCELL ASIA PACIFIC INC.

PR (RPRG-) RPR GENCELL ASIA PACIFIC INC.

XX (Sequence 7996 BP; 2463 A; 2015 C; 1829 G; 1689 T; 0 other;

XX (Sequence 7996 BP; 2463 A; 2015 C; 1829 G; 1689 T; 0 other;
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Query Match 2.8%; Score 106.8; DB 20; Length 7996; Best Local Similarity 47.1%; Pred. No. 5.8e-14; Matches 327; Conservative 0; Mismatches 367; Indels 0; Gaps 0;
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                                                                                     ttaatatacacataagtattatacacccatttttgcagtcataaaattatgcaatttcag 361
                                                                      gtttcatgttttatttcattttctttacttttagggtaaaaccaatgcccccaattcat 181
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        The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an
                                                                                                                                                                                                                                                                                                                                                  06-APR-2000;
07-APR-2000;
30-JUN-2000;
                                                                                                                                                                                           Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
                                                                                                                                                     Claim 1; SEQ ID No 459;
                                                                                                                                                                                                                                                     WPI; 2001-602752/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; tumour suppressor gene; onc cancer; tumour; CpG dinucleotide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytosine methylation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumour suppressor gene derived
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2000DE-1019173.
2000DE-1032529.
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diseases associated with CpG dinucleotides
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 e.g
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3724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the 333 genomic sequences derived from tumour suppressor genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                   3604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electron format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6292 BP; 1736 A; 99 C; 1304 G; 3153 T;
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Pred. No. 2.3e-13;
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antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
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                                                                                                                                                                     1906
                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myelo leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytosine
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for diagnosis and treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                             diseases. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rheumatoid arthritis,
                      202
                                                                                                                                                                                                                      82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention provides a number of human immune system associated es which are modified by the methylation of cytosines. The sequences be used in the diagnosis and treatment of immune system disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens.
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                    gttttatactagtttcagttttattattgtttattaagtgtttttagttggttttctcat 261
                                                                  283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune system disease; cytosine methylation;
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                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                         14006 BP; 3278 A; 155 C; 3257 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 methylation
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2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       zheimer's disease, AIDS, epilepsy, neurofibromatosis thritis, psoriasis and inflammatory/ulcerative bowel present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                           2.7%;
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ment of diseases associated
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psoriasis; bowel dis
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07-APR-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                                      human immunodeficiency virus; neurodegenerative disorder; solid tumour; graft-versus-host disease; glomerular disease; Lewy body disease; cancer; arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic;
                                                                                                                                                                                                                                                                                                                   Chemically pretreated complementary DNA associated with cell cycle #26
                                                                                                                                                                                                                                                                                           Cell cycle; human; CpG dinucleotide; cytosine methylation; HIV; human immunodeficiency virus; neurodegenerative disorder; solid
                                                                                                                                                                                                                                                                                                                                                                               AAS45347
                                                         WPI; 2001-602751/68.
                                                                                                                                                                         15-MAR-2001; 2001WO-EP02945
                                                                                                                                                                                            20-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                           Piepenbrock
                                                                                                               ; 2000DE-1013847.
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associated

cytosine methylation state e.g. arthritis, arteriosclerosis comprising fragments of cl

chemically cancer, aging

cycle

Designing primers and probes for analysing diseases associated with

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Best Local
            26-MAR-2002
                                       ABL33697;
                                                                ABL33697 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft-versus-host disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CpG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9539 BP; 2078 A; 121 C; 2281 G; 5059 T; 0 other;
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                                                                                                                                      579 tttttttttttatttttttatatattttat 610
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2867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6668 BP; 1329 A; 328 C; 1736 G; 3274 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                              404 tttattttcttctttaagggtaataccaatgatactaatttatgcctcatttggaaattt 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                       104 titotitigtaatigitigititoatgititiatiticatititotitiacitititagggiaaaa 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immune system associated gene SEQ ID NO: 1670
                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 48.8%;
                                                            aaaattatgcaatttcagtacaaattgtgcgcaaactcttcttcattttttattttat 403
                                                                                                                             9999t9t9t9t9c9t9t9ttaatatacacataagtattatacacccatttttgcagtcat
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                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                        Score 101.2; DE Pred. No. 1e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 6668;
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The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific analysing the cytosic parameters for the diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-2000;
07-APR-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS46686;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour suppressor gene derived chemically modified sequence #409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytosine methylation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS46686 standard; DNA; 7442 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        464 cgttttgaaaattatgctagtacacacttattcttgtatattatggaaaagcgcaatttc 523
                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 409; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                  Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-602752/68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-MAR-2001; 2001WO-EP02955.
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                                                                                                                                                                                                                                                                                                                                                  analysing diseases associated with cytosine methylation state e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumour;
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by analysing cytosine methylations. The parameters
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; 2000DE-1019173.
; 2000DE-1032529.
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ABL32527

ABL32527 standard; DNA; 7571 BP

26-MAR-2002 (first entry)

ABL32527;

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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7442 BP; 1655 A; 214 C; 1934 G; 3636 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2089
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2569 ttttt 2573
                                                                                                                                                                                                                                                                                                                                                                                                                   301 gttaatatacacataagtattatacacccatttttgcagtcataaaattatgcaatttca 360
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                              661 tcttt 665
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                                                                                 tottgottagaaaactttagtattttgattgtgtttttagtttttatttcattttgtttct 660
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                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.8%;
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4.2e-12;
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arterioscierosis anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatoryVulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2608
                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 500; 32pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumattc; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytosine methylation
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01-SEP-2000; 2000DE-1043826.
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Pred. No.
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Search completed: July Job time: 17362 sec 2002, 14:11:05

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           999acaccagcgtcatctccgaggtatatatccgccacatgaattatcacaattcacatg
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                                                                                                                                                                                                                                                                                                                                                                                                                                 tcgac 3785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aggccaacggtcaccgggtcatggtcatctccccgcgctacgaccagtacaaggacgcct 3600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGAC
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Murai J., Taira,T. and Ohta,D.
Direct Submission
Submitted (10-NOV-1998) Jun Murai, Osaka Prefectur
College of Agriculture; 1-1 Gakuen-cho, Sakai, Osa
Japan (E-mail:junki@demeter.plant.osakafu-u.ac.jp,
Tel:81-722-54-9409, Fax.81-722-54-9409)
                                                                                                                                                     Isolation and characterization of the three Waxy granule-bound starch synthase in hexaploid wheat Gene 234 (1), 71-79 (1999)
                                                                                                                                                                                                                                                           starch synthase (GBSSI).
Triticum aestivum DNA.
Triticum aestivum
                                                                                                                                                                                                                   Spermatophyta; Magnoliophyta; Pooideae; Triticeae; Triticum.
                                                                                                                                             99321800
                                                                                                                                                                                                                                                                                                 AB019622
AB019622.1 GI:4760579
                                                                                                                                                                                                                                                                                                                        Triticum aestivum gene for starch synthase
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/organism="Triticum aestivum"
/db_xref="taxon:4565"
                                     Location/Qualifiers
                                                                                                                                                                                         Taira, T. and Ohta, D.
                          . 2805
                                                                                                                                                                                                                                                                                                                                      2805 bp
                                                                                                                                                                                                                              Streptophyta; Embryophyta; Tracheophyta; yta; Liliopsida; Poales; Poaceae;
                                                                       Osaka Prefecture University,
-cho, Sakai, Osaka 599-8531,
                                                                                                                                                                                                                                                                                                                                       DNA
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                                                                                                                                                                           genes
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601 CGAGAGGGTGAGGTACTTCCACTGCTACAAGCGCGGGGTGGACCGCGTGTTCGTCGAC

658

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BASE COUNT
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                           3728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   μ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTGCGCGCCCATGGCGGCTCTGGTCACGTCCCAGCTCGCCACCTCCGGCACCGTCCTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agcgtcaccgacagattccggcgtccaggttttcagggcctgaggccccggaacccggcg 3247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGTCACCGGGTCATGGTCATCTCCCCGCGCGTACGACCAGTACAAGGACGCCTGGGACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACGTCCTCGGGGGGCCTCCCCGCCGCCATGGCCGTAAGCTTGCGCCACTGCCTTCTTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gacgtcctcgggggcctccccgccgccatggccgtaagcttgcgccactgccttcttata 3487
cgagagggtgaggtacttccactgctacaagcgcggggtggaccgcgtgttcgtcgac 3785
                                                                                                acatttctgcaagactttactgactggctggatctcgcagatccaaggtcgttgacaggta 3727
                                                                                                                                                                                           cagcgtcatctccgaggtatatatatccgccacatgaattatcacaattcacatgctcctgc 3667
                                                                                                                                                                                                                                                                                           cggtcaccgggtcatggtcatctccccgcgctacgaccagtaccaggacgcctgggacac 3607
                                                                                                                                                                                                                                                                                                                                                               AATGTTTCTTCCTGCAGCCATGCCTGCCGTTACAACGGGTGCCGTGTCCGTGCAGGCCAA 420
                                                                                                                                                                                                                                                                                                                                                                                           aatgtttcttcctgcagccatgcctgccgttacaacgggtgccgtgtccgtgcaggccaa 3547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGAACCTCGTGTTCGTCGGCGCCGAGATGGCGCCCTGGAGCAAGACTGGCGGCCTCGGC
                                                                         CAGCGTCATCTCCGAGGTATATATCCGCCACATGAATTATCACAATTCACATGCTCCTGC 540
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pDRFKSSFDFIDGYDKFVEGRKLNWMKAGILADTNVLTVSPYYAEELISGEARGCELD
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VEGKTGFHMGRLSVDCNVVEPADVKKVTYTLKRAVKVVCTPAXHEMVKNCMIQDLSWK
GPAKNWEDVLLELGVEGSEPGIVGEEIAPLALENVAAP"

77 a 817 c 826 g 585 t
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7gene="waxy"

1016. .496,581. .679,789. .942,1068. .1168,

1016. .1621,1713. .1892,1988. .2179,2270. .2356,2455. .2583,

1268. .1621,1713. .1892,1988. .2179,2270. .2356,2455. .2583,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="starch synthase (GBSSI)"
/protein_id="BAA77350.1"
/db_xref="GI:4760580"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(13. .333,416.
1268. .1621,1713. .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . .496,581 .679,789 .942,1068 .1168, .1892,1988 .2179,2270 .2356,2455 .2583,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                             Matches 644;
                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                  Best Local Similarity
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                                                                                                                                                                   3140 atggcggctctggtcacgtcccagctcgccacctccggcaccgtcctcagcgtcaccgac 3199
61
                                                                                                                                       1 ATGCCGCTCTCGGTCACGTCCCAGCTCGCCACCTCCGGCACCTCCTCAGCGTCACCGAC 60
                                                AGATTCCGGCGTCCAGGTTTTCAGGGCCTGAGGCCCCGGAACCCGGCGGATGCGGCGCTC 120
                                                                        agattcoggogtccaggttttcagggocotgaggococggaaccoggoggatgoggogotc 3259
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Triticum turgidum subsp.
(GBSSI), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Triticum turgidum subsp. dicoccoides (sub_species:dicoccoides) DNA.
Triticum turgidum subsp. dicoccoides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-JUN-1999) Jun Murai, Osaka Prefecture University, College of Agriculture: 1-1 Gakuen-Coho, Sakai, Osaka 599-8531, Japan (E-mail: junki@demeter.plant.osakafu-u.ac.jp, Tel:81-722-54-9409, Fax:81-722-54-9409)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolation and characterization of the four Waxy genes granule-bound starch synthase in tetraploid wheats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            starch synthase (GBSSI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                  569
                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                  KVRAVVRFNAPLAHOMMAGADVLAVTSRFEPCGLIQLQGMRYGTPCACASTGGLVDTIVEGKTGFHMGRLSVDCNVVEPADVKKVVTTLKRAVKVVGTPAYHEMVKNCMIQDLSWKGPAKNMEDVLLELGVEGSEPGIYGEEIAPLALENVAAP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HPCFLEKVRGKTKEKIYGPDAGTDYEDNQQRFSLLCQAALEVPRILDLNNNPHFSGPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="starch synthase (GBSSI)"
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/db_xref="GI:6624281"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIMRLTGITGIVNGMTVSEWDDIKDKFLTVNYDVTTALEGKALNKEALQAEVGLPVDR
KVPLVAFIGRLEEQKGPDVMIAAIPEIVKEEDVQIVLLGTGKKKFERLLKSVEEKFPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(1. .321,404. .484,569. .667,777. .930,1056. .1156,
1256. .1609,1701. .1880,1976. .2167,2258. .2344,2443. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(1. .321,404. .484,569. .667,777. .930,1056. .1156,
1256. .1609,1701. .1880,1976. .2167,2258. .2344,2443.
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/db_xref="taxon:85692"
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                                                                                                                                                                  Direct Submission
Submitted (16-JUN-1999) Jun Murai, Osaka Prefecture University,
College of Agriculture, 1-1 Gakuen-cho, Sakai, Osaka 599-8531,
Japan (E-mail:junki@demeter.plant.osakafu-u.ac.jp,
Tel:81-722-54-9409, Fax:81-722-54-9409)
                                                                                                                                                                                                                                                                                                                                            AB029063.1 GI:6624284
starch synthase (GBSSI).
Triticum durum DNA.
Triticum turgidum subsp. durum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                  App1
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Isolation and characterization of the four Waxy ger granule-bound starch synthase in tetraploid wheats Appl. Biol. Sci. (1999) In press
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Triticum durum waxy
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                        /gene="waxy"
join(1. .321,404. .484,569. .(
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1256. .
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/db_xref="taxon:4567"
2665. .2781)
/gene="waxy"
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Hordeum vulgare BAC 259116,
AF474373
AF474373.1 GI:18652401
                                                  AF474373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="starch synthase (GBSSI)"
/protein_id="BAA88511.1"
/db_xref="g1:662428"
/translation="MAALVTSQLATSGTVLSVTDRFRRPGFQGLRPRNPADAALGMRT
/translation="MAALVTSQLATSGTVLSVTDRFRRPGFQGLRPRNPADAALGMRT
VGASAAPROSKRPHRGHRCLSMVVRATGSGGMNLVFVGARAPWSKTGGLGDVLGGL
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HPCFLEKVRGKYTKKIYGPDAGTDYEDNQORFSLLCQAALEVPRILDLNNUMPHSGAPY
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PDRFKSSFDFIDGYDKFVFGFKINWMKAGILQAAKVLTVSPYYABELISGBARGCELD
NIMRLTGITGINGMDVSEWDPYKDKFITTVNYDVTTALEGKALMAEALQAEVGLPVBR
KVPLVAPIGRLEEQKGPDVMIAAIPEIVKEEDVQIVLLGTGKKKFERLLKSVEERKFPT
KVRAVVERNAPLAHQMMAGADVLAVTSRFEFGLIQGIVGTEKKFFCACASTGGLVDTI
VEGKTGFHMGRLSVCONVEYBADVKKVTTTLKRAVKVGTPAYHEMVKNCMIQDLSWK
GPAKNWEDVLLELGVEGSEPGIVGEEIAPLALENVAAP"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jiang, Z., Busso, C.S., Kleinhofs, A., Devos, K.M., Ramakrishna, W. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ma, J., SanMiguel, P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            maize, pearl millet, rice, sorghum and diploid wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Comparative sequence analysis of Wx1 homologous regions in barley,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bennetzen, J.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jiang, Z., Busso, C.S., Kleinhofs, A., Devos, K.M., Ramakrishna, W. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hordeum vulgare
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    barley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(6912. .6997,7144. .7232,7460. .
8287. .8367,8772. .8832,8944. .8975)
/gene="259116.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative leucine aminopeptidase"
/protein_id="AAL77104.1"
/protein_id="AAL77104.1"
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MGGGTWRKAYGALNDTASTRNFGTWRAYGAN
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<6912. .>8975
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8287..8367,8772..8832,8944..>8975)
/gene="259116.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCSIGWTAEARRGDNTNAEGRLTLADALVYACNQGVDKIIDLATLTGACVVALGPSIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNHVECPPKERHFRTSVNPPHFIHLCYKPVGGNVKRKLAIVGKGLTFDSGGYNIKTGP
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/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mnhakekykdaasaakakakiTQakvaekteaatarsHDereLa
HERGKAKVAAAEAELHQAKLTATARVAKSATSNEIDAVDEAVGKLAAVLDTSGEGEGA
TLKESALRAATQGAVEAGVGLRGLVLLAASSHDQFEAETDEVVRHGHRERRRWGTASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cultivar="Merex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /, West Lafayette,
location/Qualifiers
                                                                                                                                                                                                 /gene="259I16.2b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAL77105.1"
/db_xref="GI:18652403"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="259I16.2a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(10203. .10391,11938.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="259I16.2a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="259I16.2a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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/protein_id="AAL77106.1"
                                          /product="unknown"
                                                                                    /codon_start=1
                                                                                                                          join(15600. .15852,16734. .16939)
/gene="259116.2b"
                                                                                                                                                                                                                                                                                 /product="unknown"
                                                                                                                                                                                                                                                                                                                                /gene="259I16.2b"
                                                                                                                                                                                                                                                                                                                                                                 join(<15600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGRSSAIVPLDRPLCFSSLLTAEICMAPFGLGRVHVVGQPLIQSHMGKNQKRKRKNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .>12408
                                                                                                                                                                                                                                                        .>16939
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                                                                                                                                                                                                                                                                                                                                                                      .15852,16734. .>16939)
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repeat_region
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/translation="mdasilepvTlevaha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HERGKAKVAAAEAELYQAKVTHREEAMEHRLHKRGHKHSGDVDLINALIFVNLCCYQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transposon="LTR-retrotransposon Sukkula_solo" 65014. .65035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(57099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(23173, .26525)
/note="similar to putative non-LTR retrotransposon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transposon="MITE"
join(<18744. .19118,21680. .>22075)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="G1:18652404"
/translation="mnlakekvkdaasaakakakithakvaekteaatarshderela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGRSFFTEEDERWFDIWLSTSDDTNDDDDGVDDWSDWD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="hypothetical protein"
/protein_id="AAL77108.1"
/db_xref="GI:18652406"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="259116.4"
70375. .70971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
<70375. .>70971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(64715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_unit=tg
58592. .5866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58573. .58591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to mudrA-like transposon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transposon="LTR-retrotransposon BARE-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(37482. .46140)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transposon="LTR-retrotransposon BARE-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28545. .37482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transposon="MITE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20238. .20342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NSRWGGDESGRRGGWGRDGVNVQRTEAGARNKRRAMPF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="259I16.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="259I16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein"
<18744. .>22075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="259I16.3"
                                                                                                                                                                                                                             join(<72864...73181,73270...73350,73435...73533,73660...73813,
73950...74050,74165...74518,74611...74790,74885...75076,
75159...75245,75343...75471,75548...>75664)
/gene="259116.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72677. .72709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARAFDAAAWRLGRLRRQINFQDVHTLQQALDVAPPPRVNSAQDRADHTARQRRLLVAQ
EDERVMAEWRRRHPEDVAYEQGYWARRREEDTRRRREERLDRRRRKALASAHADIVNA
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                                                                         <72864. .>75664
/gene="259116.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transposon="MITE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="repetitive sequence RP-l"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=
                                                                                                                                         /product="granule-bound starch synthase"
<72864. .>75664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MPPRRRSASGYRGVRERPNGGFYAEIRSGDLRLSLGTYDTAHEA/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="259I16.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="259I16.4"
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jóin(72864. .73181,73270. .73350,73435. .73533,73660. .7
73950. .74050,74165. .74518,74611. .74790,74885. .75076
                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_unit=gaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _unit=gaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .64565
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Query Match
Best Local Similarity
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                                                                   72142 CCACTCAACAACAACAACACTCACTCACTCACGAGTGCCCCGCGACTGTGAGCACGCGCG 72201
                                                                                                                                                                                                                                                           72022
                                                                                                                                                                                                                                                                                                                                                     71963
2252 ccttgagtcccgtcactttcgcccgcccgcccacacactacaaccaggagcctcgatct 2311
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                                                                                                                                                           GCATGCATACATGCACGAGGAGCGGAGCGGGGGTATTGGGGGAT-CGGGCACCACGGG
                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transposon="MITE"
83418. .84091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="unknown"
/protein_id="aal77110.1"
/protein_id="aal77110.1"
/db_xref="GI:18652408"
/translation="massarahasaarsalrraplaasssssaaagaagilrrsaaag
LATRVPLHSAARLGSCYTRDGNNAFSNNSRRWFSSNEKHLPPISDPEIETAFKDLMAA
SWNELPGSLYEEAKKEVSKATDDKAGQEALENVFRAAEACEEFSGVLYTLRMALDDLC
GLTGENVGPLFGYLEEAVKSAYSRYMTYLESFGPEEHYLRKKVETELGTKNIHLKMRC
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[GASAAPRQSRKAHRGSRCLSVVVRAJGSGMNLVFVQAEMAPWSKTTGGLGDVLGGLP
PAMAANGHRWAVVSPRVDQXKDAMDTSVISEIKVADEYERVRFFHCYKGVDRVFIDH
PWFLEKVRGKTKEKIYGPDAGTDYEDNQORFSLLCQAALEAPRILNLIMNPYFSGPY
EDVVFVCNDWHTGLLACYLKSNYQSNGIYRTAKVAFCIHNISYGGRESEDDRAQLNLP
DRFKSSFDFIOGYDKYBCGRKINWMKAGILQADKVLTVSFYAEELISGAARGCELDN
IMRLTGITGIVNGMDVSEWDPTKDKFLAVNYDITTALEAKALMKEALQAEVGLDVDRK
VPLVAFIGRIEGEKGDDVMIAAIPEILKEEDVQIILLGTGKKKFEKLLKSMEEKFPGK
VPLVAFIGRIEGEKGDDVMIAAIPEILKEEDVQIILLGTGKKKFEKLLKSMEEKFPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="hypothetical protein"
<91421. .>92153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85127.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transposon="MITE"
join(<91421. .9151)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGIGSEWGKITLIGTSGISGSYVEMRA"
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79967...80040,80132...80247))
/gene="259116.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(<77035..77091,78213..78398,78548..78852,
79967..80040,80132..>80247))
/genpe="259116.6"
/product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VRAVVRENAPLAHOMMAGADLLAVTSREEPCGLIOLOGMRYGTPCVCASTGGLVDTIV
EGKTGFHMGRLSVDCNVVEPADVKKVATTLKRAVKVVGTPAYQEMVKNCMIQDLSWKG
PAKNWEDVLLELGVEGSEPGIVGEEIAPLAMENVAAP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="259I16.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(<77035. .>80247)
/gene="259I16.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="259I16.7"
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/protein_id="AAL77109.1"
/db_xref="GI:18652407"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="259116.
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.8%;
65.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .85346
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                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 560.2; DB 8
Pred. No. 2.8e-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .91518,91736. .>92153)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  starch synthase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 8;
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                                          3433
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CCTCGGCGGCCTCCCCCGGCCATGGCCGTAAGCTAGCATCACGACACCCAACCACCATT
                   | cctcggggggcctccccgccgccatggccgtaagcttgcgccactgc-----cttcttat 3486
                                                                    CCTCGTGTTCGTCGGCGCCCAGATGGCGCCCTGGAGCAAGACCGGCGGCCTTGGCGATGT
                                                                                        cctcgtgttcgtcggcgcgagatggcgccctggagcaagactggcggcctcggcgacgt 3432
                                                                                                                                                                                                                                     --gegecatggeggetetggteacgteecagetegecaccteeggeaccgteeteagegt
                                                                                                                                                                                                                                                                                                                                                                                                                                                        actact--cactaacaatcagtgcagtcgtctcttgctgcaggtagccacaccctgcgc- 3134
                                                                                                                                           CCGCGGGAGCCGGCGGTGCCTCTCCGTGGTGGTGCGCGCCACGGGCA---GCGGCATGAA
                                                                                                                                                              ccgattcgaccggcggtgcctctccatggtggtgcgcgccacgggcagcggcggcatgaa 3372
                                                                                                                                                                                                                GGCGCTTGGTATGAGGACTATCGGAGCAAGCGCCGCCCCGAAGCAAAGCCGGAAAGCGCA
                                                                                                                                                                                                                                                                                         CACCGACAGATTCCGGCGTCCAGGTTTTCAGGGCCTCAGGCCCCGGAACCCCGGCGGATGC
                                                                                                                                                                                                                                                                                                              caccgacagattccggcgtccaggttttcagggcctgaggccccggaacccggcggatgc
                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTACTCACACTGACGATCAGTGCAGTCGTCTCTCACTGCAGGTAGCCACACCCTGTGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAAGAGAATTTCCCCGTTTAATGAACGGAAAAGCCGGACAAAACCGTGTACTTATGTTTGG 72736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ttattaattactaccagtgcggagacaggttcatatatactctggtcatgttaatttgga 3022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         accetacagaacaaattecattteteageeagtteeaceeegtgeacgegatttaacage 2962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGCGCCATGGCGGCTCTGGCCACGTCCCAGCTCCGGCACCGTCCTCGGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACACAGGGAACATACT-----AAGAAAATTCGTGCTTGATGTTTTCTTTTTCTAAGAAA 72636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acagaggcagcataatgcgcgcataaacatttctgttttctagccgagttggatcaaaca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (21-JUN-1988) Zohde W., Max Planck Institute, Erwin Baur Institut, D-5000 Koln 30, FRG 2 (bases 1 to 5153)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rohde, W., Becker, D. and Salamini, F. Structural analysis of the waxy locus from HC Nucleic Acids Res. 16 (14B), 7185-7186 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poddeae; Triticeae; Hordeum.

1 (bases 1 to 5153)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HVWAXYG 5153 bp DNA linear PLN 10-FEB-1999 Barley DNA for waxy locus encoding starch synthase (EC 2.4.1.11).
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                                                                                                                                                                                                                /number=1
990. .154
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1549. .19
                                                                                                             join(1590. .1907,1997. .2077,2162. .2260,2387. .2540,
2677. .2777,2884. .3237,3330. .3509,3604. .3795,3878. .3964,
4062. .4190,4267. .4383)
                                                                                                                                                                                                                                                                                                                                                                   /organism="Hordeum vulgare"
/strain="Vogelsanger Gold"
/db_xref="taxon:4513"
                             /product="starch synthase"
/protein_id="CAA30755.1"
/db_xref="GI:295809"
/db_xref="SWISS-PROT:P09842"
                                                                                                                                                                                                                                                                                                /cell_line="Vogelsanger Gold 519/15"
/tissue_type="leaf"
                                                                                                                                                                /number=2
                                                                                                                                                                                                                                                                                                                                clone="lambda wx2"
                                                                                                                                                                                                                                                                                                                                                   /map="chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
/translation="maalatsqlatsgtvlgvtdrfrrpggglrprnpadaalgmrt
IGASAAPKQSRKAHRGSRRCLSVVVSATGSGMNLVFVGAEMAPWSKTGGLGDVLGGLP
                                                                                                 codon_start=1
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1572 CACCCTGTGCGCGCGCCATGGCGGCTCTGGCCACGTCCCAGCTCGCCACCTCCGGCACC

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ORIGIN
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                                               1512 TATTTACTTCACTACTCACACTGACGATCACGTCCAGTCGTCTCTCACTGCAGGTAGCCA
                                                               3070 --tttacttcactactcac---taacaatcagtgcagtcgtctcttgctgcaggtagcca 3124
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PWFLEKVRGKTKEKIYGPDAGTDYEDNQORFSLLCQAALEARRILNILNINPYESGPYG
EWFLEKVRGKTKEKIYGPDAGTDYEDNQORFSSLLCQAALEARRILNILNINPYESGPYG
EDVVEVCNDWHTGLLACYLKSNYQSNGIYRTAKVAFCIHNISYGGRFSFDDPAOLLILP
DRFKSSFDFIDGYDKFVEGRKINWMKAGILQADKVLTVSPYYAEELISGEARGCELDN
IMRLTGITGIYNGMDYSEWDPYKDKFLAVNYDITTALEAKALMKEALQAEVGLEVDRK
VPLVAFIGITLEEDKGPDVMIAAIPEILKEEDVOJIILJGKKKKEEKLLKSMEEKFPGK
VPLVAFIGRLEEDKGPDVMIAAIPEILKEEDVOJIILJGLGKKKKEEKLLKSMEEKFPGK
VRAVVERNAPLAHQMMAGADLLAVTSRFEEPCGLIQLGCMRYGTPCVCASTGGLVDTIV
EGKTGEHMGRISVDCNVVEPADVKKVATTLKRAVKVGTPAYQEMVKNCMIQDLSWKG
EKTGEHMGRISVDCNVVEPADVKKVATTLKRAVKVGTPAYQEMVKNCMIQDLSWKG
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3510. .360
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3238. .332
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2778. .28
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2677 . . 27
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4267. .>43
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3796. .387
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2387. .25
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1997. .20
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1908. .1996
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2677. .2777,2884. .3237,3330.
4062. .4190,4267. .4377)
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join(<32. .352,443. .523,620. .718,823. .976,1128. .1228,

1370. .1723,1809. .1988,2071. .2262,2347. .2433,2532. .2660,

2777. .>2893)
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<32. .>2893
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/note="GBSSI"
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2777. .2893)
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Pred. No. 1.8e-89;
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32. .2660,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-DEC-1998) School of Life Sciences and Technology, Victoria University of Technology, Werribee Campus, PO Box 14428 MCMC, Melbourne, Victoria 8001, Australia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yan, L., Bhave, M., Fairclough, R., Konic, C., Rahman, S. and Appels, R Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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<32. .>2834
                           KGPAKNWEHVLLELGVEGSEPGIVGEEIAPLAMENVAAP"
834 c 831 g 591 t
                                                                                                         SKVRAVVRFNAPLAHQMMAGADVLAVTSRFEPCGLIQLQGMRYGTPCACASTGGLVDT
                                                                                                                                                                                   DHPCFLEKYRGKTKEKIYGPDAGTDYEDNQLRFSLLCQAALEVPRILDLNNNPYFSGP
YGEDVVFVCNDWHTGLLACYLKSNYQSNGIYRTAKVAFCIHNISYQGRFSFDDFAQLN
LPDRFKSSFDFIDGYDKPVEGRKINWMKAGILQADKVLTVSPYYAEELISGEARGCEL
                                                                                                                                                                                                                                                            /translation="maalvTsQLATSGAVLGITDRFRRAGFQGVRPRSPADAALGMRT
VGASAAPKQQSRKAHRGTRRCLSVVVRATGSGGMNLVFVGAEMAPWSKTGGLGDVLGG
LPPAMAANGHRVMVISPRYDQXKDAWDTSVVSEIKVADEXERVRYEHCFKRGVDRVFV
                                                                                                                                                                                                                                                                                                                                        /product="granule-bound starch synthase WX-TmA protein"
/protein_id="AAF06936.1"
/db_xref="GI:6318538"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(32. .355,444. .524,613. .711,830. .983,1127. .1227,
1309. .1662,1752. .1931,2013. .2204,2288. .2374,2474. .2602,
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                                                                                 IVEGKTGFHMGRLSVDCNVVEPADVKKVVTTLKRAVKVVGTPAYHEMVKNCMIQDLSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3694 gctggatctcgcagatcaaggtcgttgaccaggtacgagagggtgaggtacttccactgct 3753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 GAGCAAGACCGGCGGCCTCGGCGACGTCCTCGGGGGCCTCCCCCAGCCATGGCCGTAAG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GAGGCCCCGGAGCCCGGCGGATGCGGCCCTCGGCATGAGGACTGTCGGAGCAAGCGCGGC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CACCTCCGGCGCCCTCCTCGGCATCACCGACAGGTTCCGGCGTGCAGGTTTTCAGGGCGT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ctacgaccagtacaaggacgcctgggacaccagcgtcatctccgaggt----atatatcc 3633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACAAC - - GTGCTGTGTCTATGCAGGCCAACGGTCACCGGGTCATGGTCATCTCCCCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gagcaagactggcggcctcggcgacgtcctcggggggcctccccgccgccatggccgta-- 3463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              621;
                                                                                                           Murai
                                                                                                                                              Spermatophyta; Magnoliophyta;
Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                      Triticum aestivum
                                                                                                                                                                                                                       Triticum aestivum DNA.
                                                                                                                                                                                                                                       starch synthase (GBSSI).
                                                                                                                                                                                                                                                          AB019624.1 GI:4760583
                                                                                                                                                                                                                                                                           AB019624
                                                                                                                                                                                                                                                                                           AB019624 2886 bp DNA linear Triticum aestivum gene for starch synthase (GBSSI),
Murai, J., Taira, T. and Ohta, D
                                                                       granule-bound starch synthase in hexaploid wheat
                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                   Gene 234 (1), 71-79 (1999)
                                      99321800
                                                                                        Isolation and characterization of the three Waxy genes encoding the
                                                                                                                               (sites)
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89.7%;
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                                                                                                                                                                                                                                                                                                                  2886 bp
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Best Local Similarity
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3600 tgggacaccagcgtcatctccgaggta-----tatatccgccacatgaattatcacaa 3652
                                                                                                                                                             3484 tataaatgt----ttcttcctgcagccatgcctgccgttaccaacgggtgccgtgtccgtg 3539
                                                                                                                                                                                                                                                                                                                                        3368 atgaacctcgtgttcgtcggcgcgagatggcgccctggagcaagactggcggcctcggc 3427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3128 cctgcgcgcgccatggcggctctggtcacgtcccagctcggccacctccggcaccgtcctc 3187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                               241 ATGAACCTCGTGTTCGTCGGCGCCGAGATGGCGCCCTGGAGCAAGACCGGCGGCCTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                        181 GCGCACCGCGGACCCGGCGGTGCCTCCATGGTGGTGCGCGCCACCGGCAGCGGCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CCTGCGCGCCATGGCGGCTCTGGTCACGTCCCAGCTCGCCACCTCCGGCACCGTCCTC 60
                                            CAGGCCAACGGCCACCGGGTCATGGTCATCTCCCCGCGCTACGACCAGTACAAGGACGCC
                                                                    caggccaacggtcaccgggtcatggtcatctccccgcgctacgaccagtacaaggacgc 3599
                                                                                                                                   CATAATGTTCATCTTGCAGTTGCAGCCATGCCTGCCGTTACAACGGGTGGTGTCTCCGTG
                                                                                                                                                                                                                                                    gacgtcctcgggggcctcccccgccgccatggccgtaagct----tgcgccactgccttct 3483
                                                                                                                                                                                                                            GACGTCCTCGGGGGCCTCCCCCCAGCCATGGCCGTAAGCTAGACAGCACCACTGTCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gatgcggcgctcggcatgaggactgtcggagcgagcgccgccccaaagcaaagcaaggaaa 3307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCATCACCGACAGGTTCCGGCGTGCAGGTTTCCAGGGCGTGAGGCCCCGGAGCCCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           603;
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Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submission
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PDRFKSSFDFLOGYDKPVEGRKINWMKAGILQADKVLTVSPYYAEELISGEARGCELD
NIMRLTGITGIVNGMDVSEWDPFKDKFLAKVNYDITALEGKALNKEALQAEVGLPVDR
KVPLVAFIGRLEEDKOPDVMIAAIPEILKEEDVQIVLIGTGKKKFERLLKSIEEKFP
KVRAVVRFNAPLAHQMMAGADVLAVTSRFEPCGLIQLQGMRYGTPCACASTGGLVDTI
VEGKTGFHMGRLSVDCNVVEPADVKKVVTTLKRAVKVVGTPAVHEMVKNCMIQDLSWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="waxy
join(13. .3:
1351. .1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="starch synthase (GBSSI)"
/protein_id="BAA77352.1"
/protein_id="BAA77352.1"
/db_xref="G1:4760584"
/translation="MAALUTSCLATSGTVLGTTDRFFRRAGFQGVRPRSPADAALGMRT
VGASAAPTOSRKAHRGTRRCLSMVVRATGSGGMNLVFVGAEMAPWSKTGGLGDVLGGL
VGASAAPTOSRKAHRGTRRCLSMVVRATGSGGMNLVFVGAEMAPWSKTGGLGDVLGGL
PPAMAANGHRVMVISPRYDQYXDAWDTSVVSEIKVVDKYERVRYFHCYKRGVDRVFVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPAKNWEDVLLELGVEGSEPGVIGEEIAPLAMENVAAP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HPCFLEKYRGKTKEKIYGPDAGTDYEDNQQRFSLLCQAALEVPRILNLDNNPYFSGPY
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/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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1. .1704,1790. .1969,2052. .2243,2328. .2414,2513. .2641,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Appl. Biol. Sci. (1999) In pre 2 (bases 1 to 2804)
Murai,J., Taira,T. and Ohta,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolation and characterization of the four Waxy genes encoding the granule-bound starch synthase in tetraploid wheats Appl. Biol. Sci. (1999) In press
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                     577
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                                                                                            /translation="maalvTsqlatsgtvlgItdrerrageqgyrprnpadaalvmrt
[GaSaAPERQSRKAHRGSRCLSMVVRATGSGGMILVEVGAEMAPMSKTGGLGDVLGGL
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HPCFLEKVRGKTKEKIYGPDAGTDYEDNQLRFSLLCQAALEAPRILDLNNNPYTSGPY
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PDRFKSSEDFIDGYDREVEGRKINWMAAGILQADKVLIVSPYYAEELISGEARGCELD
NIMRLTGITGIVNGMDVSEWDPTKDKFLAVNYDVTTALEGKALNKEALQAEVGLPVDR
KYPLVAFIGRLEGKGPDVMIAAIPEILKEEDVQIVLLGTGKKKEFRLLKSVEEKFPN
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VEGKTGFHMGRLSVDCNVVEPADVKKVVTTLKRAVKVVGTPAYHGMVKNCMIQDLSWK
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/protein_id="BAA88512.1"
/db_xref="GI:6624287"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="waxy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(1. .321,418. .498,590. .688,799. .952,1093. .1193,
1293. .1646,1731. .1910,1993. .2184,2265. .2351,2439. .2567,
                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                        /gene="waxy"
                                                                                                                                                                                                                                                                                                                                                                                                                               join(l. 321,418. 498,590. 688,799. 952,1093. 119: 1293. 1646,1731. 1910,1993. 2184,2265. 2351,2439.
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Best Local Similarity

13.1%;

Score 495.2; DB Pred. No. 3e-84;

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Length 2804;

Query Match

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Triticum aestivum gene for starch synthase (GBSSI), complete
AB019623
                                                                Isolation and characterization of the three Waxy genes granule-bound starch synthase in hexaploid wheat Gene 234 (1), 71-79 (1999)
                                                                                                                                                                             Triticum aestivum
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                                                                                                                                                                                                       starch synthase (GBSSI).
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           Murai, J., Taira, T. and Ohta, D. Direct Submission
                                                                                                          Murai,J., Taira,T. and Ohta,D.
                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Submitted (10-NOV-1998) Jun Murai, Osaka Prefecture University,
                                                      99321800
                                                                                                                                      Pooideae;
                                                                                                                                                  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-DEC-1998) School of Life Sciences and Technology, Victoria University of Technology, Werribee Campus, PO Box 14428 MCMC, Melbourne, Victoria 8001, Australia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome (1999) In press 2 (bases 1 to 2826)
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Aegilops speltoides

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticae; Aegilops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yan, L., Bhave, M., Fairclough, R., Konic, C., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yan,L., Bhave,M., Fairclough,R., Konic,C., Rahman,S. and Appels,R. The genes encoding granule-bound starch synthases at the waxy loci of the A, B and D progenitors of common wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aegilops speltoides granule-bound starch synthase WX-TsB protein (WX-TsB) gene, complete cds.
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                                                   SKVRAVVRENAPLAHQMMÄGADVLAVTSREEPCGLIQLQGMRYGTPCACASTGGLVDT
IVEGKTGFHMGRLSVDCNVVEPADVKKVVTTLKRAVKVVGTPAYHEMVKNCMIQDLSW
KGPAKNWEDVLLELGVEGSEPGVIGEEIAPLAMENVAAP®
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1316. .16
2710. .28
                                                                                                                                                              /product="granule-bound starch synthase
/protein_id="AAF06937.1"
/db_xref="GI:8318540"
                                                                                                                                                                                                                                                                                                                                                /organism="Aegilops speltoides"
/cullivar="AUS 21638"
/db_xref="taxon:4573"
join(<32. .355,455. .535,625. .723,837. .9331. .1316. .1669,1754. .1933,2016. .2207,2291.
                                                                                                                                                                                                       /note="GBSSI"
/codon_start=1
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Murai,J., Taira,T. and Ohta,D.
Isolation and characterization of the four Waxy genes granule-bound starch synthase in tetraploid wheats
Appl. Biol. Sci. (1999) In press
2 (bases 1 to 2793)
                                                                                                             Triticum turgidum subsp. dicoccoides (sub_species:dicoccoides) DNA. Triticum turgidum subsp. dicoccoides
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
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Triticum turgidum subsp.
                                                                                                                                                                                                                                                                          (GBSSI), complete cds AB029062
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                      3537 gtgcaggccaacggtcaccgggtcatggtcatctccccgcgctacgaccagtacaaggac 3596
                                                                                                                                                                                                             241 GTGTTCGTCGGCGCCGAGATGGCGCCCTGGAGCAAGACCGGCGGCCTCGGCGACGTCCTC 300
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419 -TGCAGGCCAACGGTCACCGGGTCATGGTCATCTCCCCGCGCTACGACCAGTACAAGGAC 477
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                                                                                                     ATGTTTCTTCTTGCAGCCAGCCATGCCTGCCATTACAAGTTTACAACTGATGCTGTGTC- 418
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RKVPLVAFIGRLEEQKGPDVMIAAIPEILKEEDVQIVLLGTGKKKEERLLKSVEEKFP
SKVEAVVERNAPLAHQMMAGADVLAVTSRFEEPGGLIGLQGMRYGTPCACASTGGLVDT
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YGEDVVFVCNDRHTGLLACYLKSNYQSSGIYRTAKVAFCIHNISYQGRESFDDFAQLN
LPDRFKSSFDFIDGYDKPVEGRKINWMKAGILQADKVLTVSPYYAEELISGEARGCEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MAALVTSQLATSGTVLGITDRFRRAGFQGVRPRSPADAPLGMRT
TGASAAPKQQSRKAHRGTRRCLSMVVRATGSAGMNLVFVGAEMAPWSKTGGLGDVLGG
LPPAMAANGHRVMVISPRYDQXKDAWDTSVVSEIKVADEVERVRYFHCYKRGVDRVFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="starch synthase (GBSSI)"
/protein_id="BAA88510.1"
/db_xref="GI:6624283"
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1262 .1615,1708 .1887,1974 .2165,2249 .2335,2433.
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87.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoding the waxy protein Plant Mol. Biol. 16 (6), 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                   /LIANSIATION="MAALVTSQLATSGTVLSVTDRERRPGFQGLRPRNPADAALGMRI
VGASAAPKQSRKPHREDBRCLSMVVRATGSGGMNLVEVGAEMAPKSKTGGLGDVLGGL
PAAMAANGHRVMVISPKYDQXKDAWDTSVISEIKVVDRYERVRTPHCYKRGVDRYFVD
HDCFLEKVRGKTKEKIYGFDAGTDYEDNQQRESLLCQAALEVPRILDLNNNPHFSGPY
AMLCRAVPRRAGEDVVFYCNDWHTGLLACYLKSNYQSNGIIRTAKVAFCHNISYQGR
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M
               FSFDDFAQLNLPDRFKSSFDFIDGYDKPVEGRKINWMKAGILQADKVLTVSPYYAEEL
                                                                                                                                                               /product="glycogen (starch) synthase"
/protein_id="CAA40509.1"
/db_xref="GI:21902"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="pcss22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /chromosome="7A, 7B, 4B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Triticum aestivum"
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{	t ISGEARGCELDNIMRLTGITGIVNGMDVSEWDPIKDKFLTVNYDVTTALEGKALNKEA}
                                                                                                                                                                                                                                                                       /gene="waxy"
                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="endosperm"
/clone_lib="lambda gt10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_line="Chinese spring"
                                                                                                                                             /db_xref="SWISS-PROT:P27736"
                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                     /EC_number="2.4.1.11"
                                                                                                                                                                                                                                                                                                                   /gene="waxy"
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l (bases 1 to 2028)

Vrinten, P., Nakamura, T. and Yamamori, M.
                                                                                                                                                 Submitted (14-DEC-1998) Crop Breeding, Tohoku National Experiment Station, Shimo-Kuriyagawa, Morioka, Iwate 020-01, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF113844 2028 bp mRNA linear PLN 20 Triticum aestivum granule-bound starch synthase precursor mRNA, Wx-Dlb allele, complete cds.
                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                         Vrinten, P.L. and Nakamura, T.
                                                                                                                                                                                                                                                Molecular characterization of waxy mutations Mol. Gen. Genet. 261 (3), 463-471 (1999) 99254805
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mutated Wx-Dl gene"
     /note="Wx-Dlb null allele of Waxy wheat; spontaneously
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOAEVGLPVDRKVPLVAFIGRLEEQKGPDVMIAAIPEIVKEEDVOIVLLGTGKKKFER
LLKSVEEKFPTKYRAVVERAPLAHQMMAGADVLAVTSRFEPGGLIQLQGMRYGTPCA
CASTGGLVDTIVEGKTGFHMGRLSVDCNVEPADVKKVVTTLKRAVKVVGTPAYHEMV
KNCMIQDLSWKGPAKNWEDVLLEIGVEGSEPGIVGEEIAPLALENVAAP®
a 638 c 694 g 387 t
                                 /gene="Wx-D1"
                                                                   /db_xref="taxon:4565"
                                                                                     /organism="Triticum aestivum"
/cultivar="Waxy"
                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:4588608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.7%;
95.4%;
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                                                                                                  agactggcggcctcggcgacgtcctcgggggcctccccgccgccatggccgtaagcttgc 3470
                                                                                                                                                                                   ocacgggcagcggcatgaacctcgtgttcgtcggcgccgagatggcgccctggagca 3410
                                                                                                                                                                                                                                                                                                                                                                                                                    CCTCCGGCACCGTCCTCGGCATCACCGACAGGTTCCGGCGTGCAGGTTTCCAGGGCGTGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                            cotcoggcacogtcotcagogtcacogacagattcoggcgtccaggttttcaggggcotga 3230
ACCGGGTCATGGTCAT 376
                                        gccactgccttcttat 3486
                                                                          AGACCGGCGCCTCGGCGACGTCCTCGGGGGCCTCCCCCAGCCATGGCCGCCAACGGCC 360
                                                                                                                                                        CCACCGGCAGCGGCATGAACCTCGTGTTCGTCGGCGCGCGAGATGGCGCCCTGGAGCA
                                                                                                                                                                                                                                                                                                                                   9900009gaacooggoggatgoggotoggoatgaggactgtoggagogagogcocc 3290
                                                                                                                                                                                                                                                  CAACGCAAAGCCGGAAAGCGCACCGCGGGGACCCGGCGGTGCCTCTCCATGGTGGTGCGCG
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a 614 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="granule-bound starch synthase precursor"
/protein_id="AAD26156.1"
/db_xref="GI:4588609"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Waxy protein; non functional"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Wx-D1"
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